GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:25:40 ; Search time 106 Seconds
(without alignments)
350.562 Million cell updates/sec

Title: US-09-918-585A-322
Perfect score: 784
Sequence: 1 MAFTFAAFCYMLALLLTAAL.....FYLLAFFYYLYGMIYVLVSS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	634	80.9	144	5	Q9BJN0	Q9bjn0 boltenia vi
2	574.5	73.3	179	11	Q9D6E1	Q9d6e1 mus musculu
3	245.5	31.3	139	11	Q9CX13	Q9cx13 mus musculu
4	203.5	26.0	141	3	Q9P6K6	Q9p6k6 schizosacch
5	186.5	23.8	157	5	Q9VQL3	Q9vql3 drosophila
6	170.5	21.7	137	10	Q8GWT5	Q8gwt5 arabidopsis
7	170	21.7	56	5	Q95Y55	Q95y55 caenorhabdi
8	164.5	21.0	146	10	Q9C7D7	Q9c7d7 arabidopsis
9	163.5	20.9	166	10	Q9LH48	Q9lh48 arabidopsis
10	159.5	20.3	126	10	Q9LQ18	Q9lq18 arabidopsis
11	141	18.0	92	4	Q9H0X8	Q9h0x8 homo sapien
12	139.5	17.8	455	10	Q9LNB1	Q9lnb1 arabidopsis
13	128	16.3	160	10	Q98RK9	Q98rk9 guillardia
14	122.5	15.6	110	10	Q9LNA7	Q9lna7 arabidopsis
15	122.5	15.6	145	10	Q9SZ74	Q9sz74 arabidopsis
16	90	11.5	249	3	Q9UTD3	Q9utd3 schizosacch
17	88.5	11.3	553	3	Q8J0F3	Q8j0f3 penicillium
18	86	11.0	259	16	Q9L6M3	Q9l6m3 s part of s
19	82.5	10.5	488	8	Q9G4C2	Q9g4c2 thraustochy
20	82	10.5	422	16	Q8YB97	Q8yb97 brucella me
21	82	10.5	422	16	Q8FX46	Q8fx46 brucella su
22	81	10.3	502	5	O62511	O62511 caenorhabdi
23	80.5	10.3	407	16	Q8EET6	Q8eet6 shewanella
24	80	10.2	805	16	Q8EPU5	Q8epu5 oceanobacil
25	79.5	10.1	2836	5	Q9U3B3	Q9u3b3 caenorhabdi
26	79.5	10.1	2846	5	Q9Y0A2	Q9y0a2 caenorhabdi
27	79.5	10.1	2847	5	Q95X74	Q95x74 caenorhabdi
28	79.5	10.1	2857	5	Q9Y0A0	Q9y0a0 caenorhabdi
29	79.5	10.1	2892	5	Q9Y0A1	Q9y0a1 caenorhabdi
30	79.5	10.1	2903	5	Q95X75	Q95x75 caenorhabdi
31	78.5	10.0	305	11	Q9JKT7	Q9jkt7 rattus norv
32	78	9.9	259	16	Q8ED68	Q8ed68 shewanella
33	78	9.9	639	17	Q9HJV0	Q9hjv0 thermoplasm
34	77.5	9.9	661	16	Q9HTR3	Q9htr3 pseudomonas
35	77	9.8	270	16	Q92UN0	Q92un0 rhizobium m
36	77	9.8	270	16	Q9RW63	Q9rw63 deinococcus
37	76.5	9.8	257	16	Q8EQG3	Q8eqg3 oceanobacil
38	76.5	9.8	354	5	O62280	O62280 caenorhabdi
39	76.5	9.8	382	8	Q9ZZR0	Q9zzr0 cyanidiosch
40	76.5	9.8	421	10	Q9SBU4	Q9sbu4 chlamydomon
41	76	9.7	559	17	Q9Y8U6	Q9y8u6 aeropyrum p
42	76	9.7	590	8	Q34192	Q34192 crithidia o
43	75.5	9.6	294	5	Q9VTI1	Q9vti1 drosophila
44	75.5	9.6	350	2	O07872	O07872 synechococc
45	75.5	9.6	498	16	Q92JI6	Q92ji6 rickettsia

ALIGNMENTS

RESULT 1
Q9BJN0
ID Q9BJN0 PRELIMINARY; PRT; 144 AA.
AC Q9BJN0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Cornichon.
GN CNIB.
OS Boltenia villosa.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Boltenia.
OX NCBI_TaxID=63515;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347415; PubMed=11455434;
RA Davidson B., Swalla B.J.;
RT "Isolation of genes involved in ascidian metamorphosis: epidermal
RT growth factor signaling and metamorphic competence.";
RL Dev. Genes Evol. 211:190-194(2001).
DR EMBL; AF329820; AAK15762.1; -.
DR InterPro; IPR003377; Cornichon.
DR Pfam; PF03311; Cornichon; 1.
DR PROSITE; PS01340; CORNICHON; 1.
SQ SEQUENCE 144 AA; 16960 MW; 69A4B594D322960C CRC64;

Query Match 80.9%; Score 634; DB 5; Length 144;
Best Local Similarity 76.2%; Pred. No. 2.6e-59;
Matches 109; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

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Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||: |::||| ||||||| ||||||||||||||||||:|||||||| ||
Db          1 MAFTFAAFCYIAAIILTAFLIFFAIWQIIAFDELKTDYKNPIDQCNSLNPLVLPEYAIHI 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              || ::|| ||:|: ||||: |::||| ||||| ||||||||:||||:| || :|||
Db         61 FFTLLFLWGGEWVTVALNMPLIGYNVWRYLHRPVMSAPGLYDPTTVMNADVLTYCMREGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVS 143
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                  |||||||::|||||| ||||||:
Db        121 CKLAFYLISFFYYLYRMIYVLVT 143


RESULT 2
Q9D6E1
ID   Q9D6E1      PRELIMINARY;      PRT;   179 AA.
AC   Q9D6E1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   2900075G08Rik protein.
GN   2900075G08RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK013789; BAB28996.1; -.
DR   MGD; MGI:1920228; 2900075G08Rik.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
SQ   SEQUENCE   179 AA;  21105 MW;  B738709483743E82 CRC64;

  Query Match             73.3%;  Score 574.5;  DB 11;  Length 179;
  Best Local Similarity   60.3%;  Pred. No. 6.3e-53;
  Matches  108;  Conservative   13;  Mismatches   23;  Indels   35;  Gaps   1;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLN---------- 49
              |||||||||||||:|:| ||||||||||||||||:||:|:|||||| ::
Db          1 MAFTFAAFCYMLSLVLCAALIFFAIWHIIAFDELRTDFKSPIDQCNPVHARERLRNIERI 60

Qy         50 ------------------------PLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYH 85
                                       |||||| ||: ||:||||| |||||||||:||| ||
Db         61 CFLLRKVRGVPPGGRRKGRRERGQQLVLPEYSIHSLFCIMFLCAQEWLTLGLNVPLLFYH 120

Qy         86 IWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLYGMIYVLVSS 144
               |||   |  |    |||  :|||| |:||||| |||||||||:|||||| ||| ||||
Db        121 FWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLLSFFYYLYCMIYTLVSS 179


RESULT 3
Q9CX13
ID   Q9CX13      PRELIMINARY;      PRT;   139 AA.
AC   Q9CX13;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   D530030D03Rik protein.
GN   D530030D03RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Stomach;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK021301; BAB32366.1; -.
DR   MGD; MGI:1925828; D530030D03Rik.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
SQ   SEQUENCE   139 AA;  16089 MW;  CA76B250D08EC091 CRC64;

  Query Match             31.3%;  Score 245.5;  DB 11;  Length 139;
  Best Local Similarity   38.0%;  Pred. No. 2.9e-18;
  Matches   52;  Conservative   24;  Mismatches   60;  Indels    1;  Gaps    1;

Qy          7 AFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |  :: :||   |||| ::: ||   :|: || |    |: ||  |:|| : |    |:
Db          3 AVVFLFSLLDCCALIPLSVYFIITLSDLECDYINARSCCSKLNKWVIPELVGHTIVTVLM 62

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
              | :  |    ||:|:  ::|:|::  |     |::||| | |   |    ||  || ||
Db         63 LVSLHWFIFLLNLPVATWNIYRFIMVP-SGNMGVFDPTEIHNRGQLKSHMKEAMIKLGFY 121

Qy        127 LLAFFYYLYGMIYVLVS 143
              || || ||| ||  |::
Db        122 LLCFFMYLYSMILALIN 138


RESULT 4
Q9P6K6
ID   Q9P6K6      PRELIMINARY;      PRT;   141 AA.
AC   Q9P6K6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Putative er-derived vesicles protein similar to yeast erv14.
GN   SPAC30C2.05.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972h-;
RA   Saunders D., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL355652; CAB90792.1; -.
DR   GeneDB_SPombe; SPAC30C2.05; -.
DR   InterPro; IPR003377; Cornichon.
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DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
SQ   SEQUENCE   141 AA;  16614 MW;  C9EEC2A6E89D1B5F CRC64;

  Query Match             26.0%;  Score 203.5;  DB 3;  Length 141;
  Best Local Similarity   33.1%;  Pred. No. 8.1e-14;
  Matches   47;  Conservative   25;  Mismatches   55;  Indels   15;  Gaps    3;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              :|:||           |  | :   |: :| | :|: || |||| || || ||:|| : |
Db         12 LAYTF--------YRLNGANMLLQIFCVIMFSDLEMDYINPIDLCNKLNDLVMPEIISHT 63

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
                :: |   :||    |:||| :|     :  |:    : | | |     |   ::: :
Db         64 LVTLLLLLGKKWLLFLANLPLLVFH-----ANQVIHKTHILDATEIFRQ--LGRHKRDNF 116

Qy        121 CKLAFYLLAFFYYLYGMIYVLV 142
               |: |||: ||  || |:  |:
Db        117 IKVTFYLIMFFTLLYCMVMSLI 138


RESULT 5
Q9VQL3
ID   Q9VQL3      PRELIMINARY;      PRT;   157 AA.
AC   Q9VQL3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CG17262 protein.
GN   CG17262.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003581; AAF51153.1; -.
DR   FlyBase; FBgn0031499; CG17262.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
SQ   SEQUENCE   157 AA;  18430 MW;  E9322CE1B06EF627 CRC64;

  Query Match             23.8%;  Score 186.5;  DB 5;  Length 157;
  Best Local Similarity   30.2%;  Pred. No. 5.6e-12;
  Matches   42;  Conservative   29;  Mismatches   61;  Indels    7;  Gaps    3;

Qy          6 AAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVM 65
              | ||  : ||:  |::   |::::   :|: || |  : :  ||  |:|::  ||  ||:
Db          7 ATFC--ITLLVYGAILLLLIYYVLTLADLECDYLNAQECCRRLNFWVIPKFGSHALLCVL 64

Qy         66 FLCAAEWLTLGLNMPLLAYHIWRY--MSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKL 123
               |    |:   ||:|::   || :  : |      |:|||  | :  :|   :     |
Db         65 LLLGGHWVMFLLNLPMV---IWLFYELHRQRRDSLGVYDPVDIHSRGLLKVHLRNCMIYL 121

Qy        124 AFYLLAFFYYLYGMIYVLV 142
              :| : ||  || :|  |:
Db        122 GYYFVMFFVGLYCLISSLI 140


RESULT 6
Q8GWT5
ID   Q8GWT5      PRELIMINARY;      PRT;   137 AA.
AC   Q8GWT5;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein.
GN   AT1G62880/F16P17_37.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
RA   Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
RA   Hayashizaki Y., Shinozaki K.;
RT   "Arabidopsis thaliana full-length cDNA.";
RL   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK118647; BAC43243.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   137 AA;  16442 MW;  A59E2EE301AB85E8 CRC64;

  Query Match             21.7%;  Score 170.5;  DB 10;  Length 137;
  Best Local Similarity   29.2%;  Pred. No. 2.4e-10;
  Matches   38;  Conservative   30;  Mismatches   55;  Indels    7;  Gaps    2;

Qy         10 YMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCA 69
              :::: |:   |:   :: :|:  :|: || || |  : :| :|||| ::  | || :|
Db          7 WIISFLILITLLGLIVYQLISLADLEFDYINPYDSASRINFVVLPESILQGFLCVFYLVT 66

Qy         70 AEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLA 129
                 |    | :| | |:   |  :        | | | | |  :| : :|:   |||: :|
Db         67 GHWFMALLCVPYLYYNFHLYSRK-----QHLIDVTEIFN--LLDWEKKKRLFKLAYIILT 119

Qy.       130 FFYYLYGMIY 139
               |  :: :||
Db        120 LFLTIFWLIY 129


RESULT 7
Q95Y55
ID   Q95Y55      PRELIMINARY;      PRT;    56 AA.
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AC   Q95Y55;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical 6.6 kDa protein.
GN   Y64H9A.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Kellen J., Gibson A.;
RT   "The sequence of C. elegans cosmid Y64H9A.";
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Waterston R.;
RT   "Direct Submission.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC006812; AAK39349.1; -.
DR   WormPep; Y64H9A.1; CE27298.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   56 AA;  6644 MW;  84A57FF87E86368A CRC64;

  Query Match             21.7%;  Score 170;  DB 5;  Length 56;
  Best Local Similarity   60.8%;  Pred. No. 1.1e-10;
  Matches   31;  Conservative    8;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          94 VMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLYGMIYVLVSS 144
               :| |||:|||||||:|    |:   :  | ||||||::|||||| ||| ||:|
Db           1 MMPGPGIYDPTTILNRSTLSSTLRISWIKLAFYLVSFFYYLYVMIYTLVTS 51


RESULT 8
Q9C7D7
ID   Q9C7D7      PRELIMINARY;      PRT;   146 AA.
AC   Q9C7D7;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 17.4 kDa protein.
GN   F28J15.3.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016720; PubMed=11130713;
RA   Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA   Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA   Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA   De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA   Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA   Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA   Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA   Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA   Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA   Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA   Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA   Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA   Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA   de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA   Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA   Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA   Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA   Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA   Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA   Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA   Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA   Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA   Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA   Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA   Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT   "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:820-822(2000).
DR   EMBL; AC069472; AAG51073.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   146 AA;  17367 MW;  975BACE86AAE22FD CRC64;

  Query Match             21.0%;  Score 164.5;  DB 10;  Length 146;
  Best Local Similarity   24.8%;  Pred. No. 1.1e-09;
  Matches   34;  Conservative   33;  Mismatches   63;  Indels    7;  Gaps    2;

Qy           8 FCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFL 67
               | ::::  :: ||:    : :|   :|: || || :    :| ||:||:::    |::||
Db           6 FLWIVSFFVSLALVASVFYQVICLTDLEADYLNPFETSTRINRLVIPEFILQGSLCLLFL 65

Qy          68 CAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYL 127
                 |:   : :|:  ||   |  |       | | | :     ::: :|  : || ||:
Db          66 LTWHWVFFLVAVPVTVYHAMLYKERRY-----LIDVTEVFRG--ISFEKKLRYTKLGFYV 118

Qy         128 LAFFYYLYGMIYVLVSS 144
                 |   :: :    | |
Db         119 FLFIMVVFRLTLSAVYS 135


RESULT 9
Q9LH48
ID   Q9LH48      PRELIMINARY;      PRT;   166 AA.
AC   Q9LH48;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Genomic DNA, chromosome 3, BAC clone: T23B7.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Columbia;
RA   Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Columbia;
RX   MEDLINE=20363099; PubMed=10907853;
RA   Nakamura Y.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT   Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT   TAC and BAC clones.";
RL   DNA Res. 7:217-221(2000).
DR   EMBL; AP002063; BAB01968.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
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SQ   SEQUENCE   166 AA;  19478 MW;  E4D7657A3F1FD77E CRC64;

  Query Match             20.9%;  Score 163.5;  DB 10;  Length 166;
  Best Local Similarity   25.0%;  Pred. No. 1.6e-09;
  Matches   32;  Conservative   32;  Mismatches   57;  Indels    7;  Gaps    2;

Qy          8 FCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFL 67
              | :::: :: ||:    : :|   :|: || || :    :| ||:||:::    |::||
Db          6 FLWIVSFFVSLALVASVFYQVICLTDLEADYLNPFETSTRINRLVIPEFILQGSLCLLFL 65

Qy         68 CAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYL 127
                |:   : :|:  ||   |  |       | | | :     ::: :|  : || ||:
Db         66 LTWHWVFFLVAVPVTVYHAMLYKERRY-----LIDVTEVFRG--ISFEKKLRYTKLGFYV 118

Qy        128 LAFFYYLY 135
               |   ::
Db        119 FLFIMVVF 126


RESULT 10
Q9LQ18
ID   Q9LQ18      PRELIMINARY;      PRT;   126 AA.
AC   Q9LQ18;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   F16P17.3 protein.
GN   F16P17.3.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Sakano H., Liu S.X., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA   Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A.,
RA   Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
RA   Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
RA   Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
RA   Ecker J.R., Federspiel N.A., Theologis A.;
RT   "The sequence of BAC F16P17 from Arabidopsis thaliana chromosome 1.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC011000; AAF75818.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
SQ   SEQUENCE   126 AA;  15114 MW;  CD61CEF886FC1827 CRC64;

  Query Match             20.3%;  Score 159.5;  DB 10;  Length 126;
  Best Local Similarity   28.6%;  Pred. No. 3.2e-09;
  Matches   36;  Conservative   29;  Mismatches   54;  Indels    7;  Gaps    2;

Qy         10 YMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCA 69
              :::: |:   |:   :: :|:  :|: || || |  : :| :|||| ::  | || :|
Db          7 WIISFLILITLLGLIVYQLISLADLEFDYINPYDSASRINFVVLPESILQGFLCVFYLVT 66

Qy         70 AEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLA 129
               |   | :| | |:   |  :       | | | | |  :| : :|:   |||: :|
Db         67 GHWFMALLCVPYLYYNFHLYSRK-----QHLIDVTEIFN--LLDWEKKKRLFKLAYIILT 119

Qy        130 FFYYLY 135
                |  ::
Db        120 LFLTIF 125


RESULT 11
Q9H0X8
ID   Q9H0X8      PRELIMINARY;      PRT;    92 AA.
AC   Q9H0X8;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein.
GN   DKFZP586E1222.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Uterus;
RX   MEDLINE=21154917; PubMed=11230166;
RA   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,
RA   Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H.,
RA   Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA   Mewes H.W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA   Wambutt R., Korn B., Klein M., Poustka A.;
RT   "Towards a Catalog of Human Genes and Proteins: Sequencing and
RT   Analysis of 500 Novel Complete Protein Coding Human cDNAs.";
RL   Genome Res. 11:422-435(2001).
DR   EMBL; AL136930; CAB66864.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   92 AA;  10615 MW;  A99857E36401B352 CRC64;

  Query Match             18.0%;  Score 141;  DB 4;  Length 92;
  Best Local Similarity   34.1%;  Pred. No. 2.1e-07;
  Matches   28;  Conservative   18;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          7 AFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |  :: :||   |||| ::: ||   :|: || |    |: ||  |:|| : |    |:
Db          3 AVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTVLL 62

Qy         67 LCAAEWLTLGLNMPLLAYHIWR 88
              | :  |    ||:|:  ::|:|
Db         63 LMSLHWFIFLLNLPVATWNIYR 84


RESULT 12
Q9LNB1
ID   Q9LNB1      PRELIMINARY;      PRT;   455 AA.
AC   Q9LNB1;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   F5O11.7.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA   Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA   Ecker J.R.;
RT   "Genomic sequence for Arabidopsis thaliana BAC F5O11 from chromosome
RT   I.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ecker J.R.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ecker J.R.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
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RA   Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA   Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA   Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA   Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA   Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA   Theologis A., Ecker J.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC025416; AAF79631.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
SQ   SEQUENCE   455 AA;  51561 MW;  D6CE7DED380BAF0C CRC64;

  Query Match             17.8%;  Score 139.5;  DB 10;  Length 455;
  Best Local Similarity   33.3%;  Pred. No. 1.5e-06;
  Matches   28;  Conservative   14;  Mismatches   37;  Indels    5;  Gaps    1;

Qy         25 IWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAY 84
              |:|::   :|: || || |  : :| :||||:::    || :|    |    | :| | |
Db         14 IFHLVCLADLEFDYINPYDSASRINSVVLPEFIVQGVLCVFYLLTGHWFMTLLCLPYLYY 73

Qy         85 HIWRYMSRPVMSGPGLYDPTTIMN 108
              :  |  |       | | | | |
Db         74 NFHLYSKR-----QHLVDVTEIFN 92


RESULT 13
Q98RK9
ID   Q98RK9      PRELIMINARY;      PRT;   160 AA.
AC   Q98RK9;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical 18.7 kDa protein orf160 from chromosome 1 (Hypothetical
DE   18.7 kDa protein orf160 from chromosome 3).
GN   ORF160.
OS   Guillardia theta (Cryptomonas phi).
OC   Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX   NCBI_TaxID=55529;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21223349; PubMed=11323671;
RA   Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
RA   Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
RT   "The highly reduced genome of an enslaved algal nucleus.";
RL   Nature 410:1091-1096(2001).
DR   EMBL; AF165818; AAK39902.1; -.
DR   EMBL; AF083031; AAK39731.1; -.
DR   EMBL; AF083031; AAK39781.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   160 AA;  18743 MW;  56BEDEF0230C7B15 CRC64;

  Query Match             16.3%;  Score 128;  DB 10;  Length 160;
  Best Local Similarity   29.4%;  Pred. No. 8.7e-06;
  Matches   32;  Conservative   22;  Mismatches   47;  Indels    8;  Gaps    3;

Qy         33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSR 92
              :| ||  ||:: |: :| | :|||| | |  : |:    |:   || | : |:  ::
Db         38 DLSTDTVNPVEVCDKVNQLKVPEYLAHLFLSIAFVIRGWWIVGFLNFPPFIFYNFAQW--- 94

Qy         93 PVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLY-GMIYV 140
                 |    |  | |  :|:   :    | ||:::   | ::  ||:|
Db         95 --YEGKHQLDSAQIFN--VLSRELRVIKAKSAFFIIIVIYTIWEWMIWV 139


RESULT 14
Q9LNA7
ID   Q9LNA7      PRELIMINARY;      PRT;   110 AA.
AC   Q9LNA7;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   F5O11.11.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
RA   Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA   Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
RA   Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
RA   Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA   Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA   Ecker J.R.;
RT   "Genomic sequence for Arabidopsis thaliana BAC F5O11 from chromosome
RT   I.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ecker J.R.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Ecker J.R.;
RL   Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
RA   Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
RA   Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA   Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA   Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA   Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
RA   Theologis A., Ecker J.;
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC025416; AAF79633.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
SQ   SEQUENCE   110 AA;  13003 MW;  8C6D066C5DDCC67D CRC64;

  Query Match             15.6%;  Score 122.5;  DB 10;  Length 110;
  Best Local Similarity   25.4%;  Pred. No. 2.3e-05;
  Matches   32;  Conservative   26;  Mismatches   45;  Indels   23;  Gaps    4;

Qy         10 YMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCA 69
              ::::     ||:   :: ::   :|: || || |  : :| :||||:::    || :
Db          7 WLISFFFLIALVGIIVYQLVCLADLEFDYINPYDSASRINSVVLPEFIVQGVLCVFY--- 63

Qy         70 AEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLA 129
                        ||  |   | |       | | | | |  :| : :|:   |||: :|
Db         64 -----------LLTGHC--YSKR-----QHLVDVTEIFN--LLNWEKKKRLFKLAYIVLN 103

Qy        130 FFYYLY 135
                | ::
Db        104 LFLTIF 109


RESULT 15
Q9SZ74
ID   Q9SZ74      PRELIMINARY;      PRT;   145 AA.
AC   Q9SZ74;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical 17.3 kDa protein.
GN   F16J13.160 OR AT4G12090.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RA   Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA   Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
RA   Mewes H.W., Lemcke K., Mayer K.F.X.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RA   EU Arabidopsis sequencing project;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL049638; CAB40950.1; -.
DR   EMBL; AL161533; CAB78252.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   145 AA;  17258 MW;  4E4B330AED9AB52D CRC64;

  Query Match             15.6%;  Score 122.5;  DB 10;  Length 145;
  Best Local Similarity   29.0%;  Pred. No. 3e-05;
  Matches   31;  Conservative   21;  Mismatches   48;  Indels    7;  Gaps    2;

Qy         33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSR 92
              :|: |  || |  : :| :||||: :    |: ::    |    |::| | |:|  || |
Db         40 DLEFDRINPYDVSSRINRMVLPEFGLQGLLCLYYILTGHWFMAVLSLPHLFYNIRLYMKR 99

Qy         93 PVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLYGMIY 139
                  | | | : | :   : ||:   |:    |: |   | :|:
Db        100 -----EHLADVTELYNTN--KWEQKKRVYKIGHIALSIFITTYWLIH 139

Search completed: September 11, 2003, 14:39:55
Job time : 109 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:36:35 ; Search time 23 Seconds
(without alignments)
294.428 Million cell updates/sec

Title: US-09-918-585A-322
Perfect score: 784
Sequence: 1 MAFTFAAFCYMLALLLTAAL.....FYLLAFFYYLYGMIYVLVSS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	784	100.0	144	1	CNIH_HUMAN	O95406 homo sapien
2	778	99.2	144	1	CNIH_MOUSE	O35372 mus musculu
3	586	74.7	160	1	CNIL_HUMAN	Q8tbe1 homo sapien
4	575	73.3	160	1	CNIL_MOUSE	O35089 mus musculu
5	548	69.9	144	1	CNI_DROME	P49858 drosophila
6	544	69.4	144	1	CNI_DROVI	P52159 drosophila
7	472	60.2	145	1	YFR3_CAEEL	Q22361 caenorhabdi
8	244.5	31.2	139	1	H163_HUMAN	Q9p003 homo sapien
9	212.5	27.1	137	1	ERV4_YEAST	P53173 saccharomyc
10	204.5	26.1	134	1	YEY5_SCHPO	O14038 schizosacch
11	193.5	24.7	142	1	YB60_YEAST	P38312 saccharomyc
12	84.5	10.8	256	1	TATC_HAEIN	P44560 haemophilus
13	82.5	10.5	802	1	YGN9_YEAST	P53121 saccharomyc
14	81	10.3	446	1	NU4M_CERCA	Q34048 ceratitis c
15	79.5	10.1	621	1	P2L2_MOUSE	Q9jlg4 mus musculu
16	78.5	10.0	305	1	T2RD_RAT	Q9jkt7 rattus norv
17	77.5	9.9	296	1	YESQ_BACSU	O31520 bacillus su
18	75.5	9.6	209	1	YIL3_YEAST	P40479 saccharomyc
19	74.5	9.5	458	1	SSU1_YEAST	P41930 saccharomyc
20	74	9.4	253	1	YDIJ_BACHD	Q9z9p4 bacillus ha
21	73	9.3	258	1	TATC_ECOLI	P27857 escherichia
22	73	9.3	363	1	CYB_TRYBB	P00164 trypanosoma
23	72.5	9.2	256	1	YM56_YEAST	Q03691 saccharomyc
24	72.5	9.2	385	1	CYB_ACACA	Q37378 acanthamoeb
25	72	9.2	381	1	CYB_NEOAL	Q9xnu4 neotoma alb
26	72	9.2	797	1	S6A5_HUMAN	Q9y345 homo sapien
27	72	9.2	799	1	S6A5_RAT	P58295 rattus norv
28	71	9.1	171	1	YB74_YEAST	P38320 saccharomyc
29	71	9.1	441	1	DIHR_ACHDO	Q16983 acheta dome
30	71	9.1	459	1	NU4M_BOVIN	P03910 bos taurus
31	71	9.1	558	1	AGP3_YEAST	P43548 saccharomyc
32	70.5	9.0	401	1	NH65_CAEEL	O45907 caenorhabdi
33	70	8.9	300	1	T2R9_MOUSE	Q9jkt4 mus musculu
34	70	8.9	390	1	O85B_DROME	Q9vhq7 drosophila
35	70	8.9	852	1	WS14_HUMAN	Q9np71 homo sapien
36	70	8.9	2039	1	CCH1_YEAST	P50077 saccharomyc
37	69.5	8.9	307	1	T2RA_HUMAN	Q9nyw0 homo sapien
38	69.5	8.9	372	1	CYB_TRYBO	Q33568 trypanoplas
39	69.5	8.9	395	1	DIHR_MANSE	P35464 manduca sex
40	69	8.8	369	1	Y316_MYCPN	Q50361 mycoplasma
41	69	8.8	557	1	OM6_CHLPS	P23701 chlamydia p
42	68.5	8.7	363	1	YRU5_CAEEL	Q09351 caenorhabdi
43	68	8.7	395	1	YN84_CAEEL	Q03613 caenorhabdi
44	68	8.7	435	1	EXOQ_RHIME	Q02729 rhizobium m
45	67.5	8.6	208	1	HIS1_THEMA	Q9x0d2 thermotoga

ALIGNMENTS

RESULT 1
CNIH_HUMAN
ID CNIH_HUMAN STANDARD; PRT; 144 AA.
AC O95406;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cornichon homolog (TGAM77).
GN CNIH OR CNIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Carcinoma;
RA Plisov S.Y., Ivanov S.V., Lerman M., Perantoni A.O.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560(2000).
RN [3]
RP SEQUENCE OF 11-144 FROM N.A.
RX MEDLINE=99227056; PubMed=10209299;
RA Utku N., Bulwin G.-C., Beinke S., Heinemann T., Beato F., Randall J.,
RA Schnieders B., Sandhoff K., Volk H.-D., Milford E., Gullans S.R.;
RT "The human homolog of Drosophila cornichon protein is differentially
RT expressed in alloactivated T-cells.";
RL Biochim. Biophys. Acta 1449:203-210(1999). Q3185 April 1
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, LIVER, SKELETAL
CC MUSCLE, PANCREAS, ADRENAL MEDULLA AND CORTEX, THYROID, TESTIS,
CC SPLEEN, APPENDIX, PERIPHERAL BLOOD LYMPHOCYTES AND BONE MARROW.
CC LOWER EXPRESSION FOUND IN BRAIN, PLACENTA, LUNG, KIDNEY, OVARY,
CC SMALL INTESTINE, STOMACH, LYMPH NODE, THYMUS AND FETAL LIVER.
CC -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC ----------

CC ----------
DR EMBL; AF104398; AAC98388.1; -.
DR EMBL; AF070654; AAD20960.1; -.
DR EMBL; AF031379; AAD32301.1; -.

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DR   Genew; HGNC:19431; CNIH.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Transmembrane.
FT   TRANSMEM      11      31       POTENTIAL.
FT   TRANSMEM      57      77       POTENTIAL.
FT   TRANSMEM     123     143       POTENTIAL.
SQ   SEQUENCE   144 AA;  16699 MW;  59BD114D24C455CD CRC64;

  Query Match             100.0%;  Score 784;  DB 1;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-68;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 2
CNIH_MOUSE
ID   CNIH_MOUSE     STANDARD;      PRT;   144 AA.
AC   O35372;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cornichon homolog.
GN   CNIH.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B6D2;
RX   MEDLINE=99147138; PubMed=10022955;
RA   Hwang S.-Y., Oh B., Zhang Z., Miller W., Solter D., Knowles B.B.;
RT   "The mouse cornichon gene family.";
RL   Dev. Genes Evol. 209:120-125(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN OOCYTES, AND AT A BASAL LEVEL IN
CC       OVARIAN SOMATIC CELLS OF 6-WEEK-OLD MOUSE. EXPRESSED IN ADULT
CC       BRAIN.
CC   -!- DEVELOPMENTAL STAGE: ABUNDANT IN FULL GROWN OOCYTE AND THE
CC       OVULATED UNFERTILIZED EGG, SHOWS A SLIGHT DECREASE 12 HOURS AFTER
CC       FERTILIZATION. TRANSCRIPTS FROM THE ACTIVATED EMBRYONIC GENOME ARE
CC       PRESENT IN THE EIGHT-CELL EMBRYO.
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF022811; AAC15828.1; -.
DR   MGD; MGI:1277202; Cnih.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Transmembrane.
FT   TRANSMEM      11      31       POTENTIAL.
FT   TRANSMEM      57      77       POTENTIAL.
FT   TRANSMEM     123     143       POTENTIAL.
SQ   SEQUENCE   144 AA;  16713 MW;  DF66786D24C455CA CRC64;

  Query Match             99.2%;  Score 778;  DB 1;  Length 144;
  Best Local Similarity   99.3%;  Pred. No. 5.7e-68;
  Matches  143;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSAPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 3
CNIL_HUMAN
ID   CNIL_HUMAN     STANDARD;      PRT;   160 AA.
AC   Q8TBE1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Cornichon-like protein.
GN   CNIL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Ninomiya K., Wagatsuma M., Kanda K., Kondo H., Yokoi T., Kodaira H.,
RA   Furuya T., Takahashi M., Kikkawa E., Omura Y., Abe K., Kamihara K.,
RA   Katsuta N., Sato K., Tanikawa M., Yamazaki M., Sugiyama T., Irie R.,
RA   Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA   Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA   Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Murakawa K.,
RA   Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA   Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ---------------------------------------------------------------------
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IDS

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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AK096312; BAC04760.1; -.
DR   EMBL; BC022780; AAH22780.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; FALSE_NEG.
KW   Transmembrane.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     73     93       POTENTIAL.
FT   TRANSMEM    139    159       POTENTIAL.
SQ   SEQUENCE   160 AA;  18976 MW;  CF7E8645A9587504 CRC64;

  Query Match             74.7%;  Score 586;  DB 1;  Length 160;
  Best Local Similarity   68.1%;  Pred. No. 1.7e-49;
  Matches  109;  Conservative   11;  Mismatches   24;  Indels   16;  Gaps    1;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCN---------------- 46
              |||||||||||||:|:| ||||||||||||||||||:||:|:||||||
Db          1 MAFTFAAFCYMLSLVLCAALIFFAIWHIIAFDELRTDFKSPIDQCNPVHARERLRNIERI 60

Qy         47 --TLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPT 104
                 |  |||||| ||: ||:||||| ||||||||:||| || |||    |  |     |||
Db         61 CFLLRKLVLPEYSIHSLFCIMFLCAQEWLTLGLNVPLLFYHFWRYFHCPADSSELAYDPP 120

Qy        105 TIMNADILAYCQKEGWCKLAFYLLAFFYYLYGMIYVLVSS 144
                :|||| |:||||| |||||||||:|||||| ||| ||||
Db        121 VVMNADTLSYCQKEAWCKLAFYLLSFFYYLYCMIYTLVSS 160


RESULT 4
CNIL_MOUSE
ID   CNIL_MOUSE     STANDARD;      PRT;   160 AA.
AC   O35089;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cornichon-like protein.
GN   CNIL.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Fetal brain;
RA   Fujimoto N., Kawamoto S., Matsubara K., Okubo K.;
RT   "Cloning of mouse homologue of Drosophila cornichon protein from 17.5
RT   dpc fetal brain.";
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX   MEDLINE=99147138; PubMed=10022955;
RA   Hwang S.-Y., Oh B., Zhang Z., Miller W., Solter D., Knowles B.B.;
RT   "The mouse cornichon gene family.";
RL   Dev. Genes Evol. 209:120-125(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN EIGHT-CELL EMBRYO, BLASTOCYST,
CC       6.5-DAY WHOLE EMBRYO, 7.5.DAY PRIMITIVE STREAK, 11.5-DAY LIMB BUD
CC       AND IN 13.5-DAY WHOLE EMBRYO. ALSO IN ADULT LUNG AND BRAIN.
CC   -!- DEVELOPMENTAL STAGE: First detected at the eight-cell stage.
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AB006191; BAA21746.2; -.
DR   MGD; MGI:1277225; Cnil.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Transmembrane.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     73     93       POTENTIAL.
FT   TRANSMEM    139    159       POTENTIAL.
SQ   SEQUENCE   160 AA;  18931 MW;  00330E5E609B28BF CRC64;

  Query Match             73.3%;  Score 575;  DB 1;  Length 160;
  Best Local Similarity   66.0%;  Pred. No. 1.9e-48;
  Matches  105;  Conservative   13;  Mismatches   25;  Indels   16;  Gaps    1;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQ---------------- 44
              |||||||||||| |:| |:|||| ||||||||||:||:||||||
Db          1 MAFTFAAFCYMLTLVLCASLIFFVIWHIIAFDELRTDFKNPIDQGNPARARERLKNIERI 60

Qy         45 CNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPT 104
              |  |  ||:||| ||  ||:||||||:|||||:||| ||:|||  ||      :||
Db         61 CCLLRKLVVPEYSIHGLFCLMFLCAAEWVTLGLNIPLLFYHLWRYFHRPADGSEVMYDAV 120

Qy        105 TIMNADILAYCQKEGWCKLAFYLLAFFYYLYGMIYVLVS 143
              :||||||| ||||| |||:||||||:|||||| |:| |||
Db        121 SIMNADILNYCQKESWCKLAFYLLSFFYYLYSMVYTLVS 159


RESULT 5
CNI_DROME
ID   CNI_DROME      STANDARD;      PRT;   144 AA.
AC   P49858; Q9V423;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Cornichon protein.
GN   CNI OR CG5855.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=95300228; PubMed=7540118;
RA   Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T.;
RT   "Cornichon and the EGF receptor signaling process are necessary for
RT   both anterior-posterior and dorsal-ventral pattern formation in
RT   Drosophila.";
RL   Cell 81:967-978(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=99403001; PubMed=10471707;
RA   Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R.G., Davis T.,
RA   Doyle C., Galle R.F., George R.A., Harris N.L., Hartzell G.,
RA   Harvey D., Hong L., Houston K.A., Hoskins R.A., Johnson G., Martin C.,
RA   Moshrefi A., Palazzolo M., Reese M.G., Spradling A.C., Tsang G.,
RA   Wan K.H., Whitelaw K., Celniker S.E., Rubin G.M.;
RT   "An exploration of the sequence of a 2.9-Mb region of the genome of
RT   Drosophila melanogaster: the Adh region.";
RL   Genetics 153:179-219(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
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RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY
CC       TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES
CC       POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE
CC       ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING
CC       EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE
CC       DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- DEVELOPMENTAL STAGE: IN EARLY STAGES, IT IS PRESENT IN THE NURSE
CC       CELL OOCYTE CLUSTER. IT IS HIGHLY EXPRESSED IN STAGE 1-6 EGG
CC       CHAMBERS, EXPRESSION CEASES DURING STAGE 7 AND CANNOT BE DETECTED
CC       IN STAGES 8 AND 9. DURING STAGE 10, IT IS REEXPRESSED IN THE NURSE
CC       CELLS.
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U28069; AAA86527.1; -.
DR   EMBL; AE003415; AAF45003.1; -.
DR   EMBL; AE003650; AAF53521.1; -.
DR   PIR; A56724; A56724.
DR   FlyBase; FBgn0000339; cni.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Developmental protein; Transmembrane.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     57     77       POTENTIAL.
FT   TRANSMEM    123    143       POTENTIAL.
SQ   SEQUENCE   144 AA;  16931 MW;  27692A3F68ECE1A9 CRC64;

  Query Match             69.9%;  Score 548;  DB 1;  Length 144;
  Best Local Similarity   66.7%;  Pred. No. 6.8e-46;
  Matches   96;  Conservative   23;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||| | || |::||:  | ||||||:|:|||||||||||||||||:||||||||||:|
Db          1 MAFNFTAFTYIVALIGDAFLIFFAIFHVIAFDELKTDYKNPIDQCNSLNPLVLPEYLLHI 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              |  ::||   || :| :|:||:||||||| :|||||||||||||::  | |    :|||
Db         61 FLNLLFLFCGEWFSLCINIPLIAYHIWRYKNRPVMSGPGLYDPTTVLKTDTLYRNMREGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
               ||| ||::||||:|||:| |:|:
Db        121 IKLAVYLISFFYYIYGMVYSLIST 144


RESULT 6
CNI_DROVI
ID   CNI_DROVI      STANDARD;      PRT;   144 AA.
AC   P52159;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cornichon protein.
GN   CNI.
OS   Drosophila virilis (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7244;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Ovary;
RX   MEDLINE=95300228; PubMed=7540118;
RA   Roth S., Neuman-Silberberg F.S., Barcelo G., Schuepbach T.;
RT   "Cornichon and the EGF receptor signaling process are necessary for
RT   both anterior-posterior and dorsal-ventral pattern formation in
RT   Drosophila.";
RL   Cell 81:967-978(1995).
CC   -!- FUNCTION: ASSOCIATED WITH GURKEN, PRODUCES A SIGNAL RECEIVED BY
CC       TORPEDO RESULTING IN A SIGNALING PATHWAY THAT FIRST ESTABLISHES
CC       POSTERIOR FOLLICLE CELL FATES AND NORMAL LOCALIZATION OF THE
CC       ANTERIOR AND POSTERIOR DETERMINANTS, LATER THEY ACT IN A SIGNALING
CC       EVENT INDUCING DORSAL FOLLICLE CELL FATES AND REGULATING THE
CC       DORSAL-VENTRAL PATTERN OF EGG AND EMBRYO (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
DR   FlyBase; FBgn0015209; Dvir\cni.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Developmental protein; Transmembrane.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     57     77       POTENTIAL.
FT   TRANSMEM    123    143       POTENTIAL.
SQ   SEQUENCE   144 AA;  16927 MW;  D0F4E65560409164 CRC64;

  Query Match             69.4%;  Score 544;  DB 1;  Length 144;
  Best Local Similarity   66.7%;  Pred. No. 1.7e-45;
  Matches   96;  Conservative   23;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||| | || |::||:  | ||||||:|:|||||||||||||||||:||||||||||:|
Db          1 MAFNFTAFTYIVALIGDAFLIFFAIFHVIAFDELKTDYKNPIDQCNSLNPLVLPEYLLHL 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              |  ::||   || :| ||:||:|||||||| :||:||||||||||::  | |    :|||
Db         61 FLNLLFLFCGEWYSLCLNIPLIAYHIWRYKNRPLMSGPGLYDPTTVLKTDTLFRNLREGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
               ||| ||::||||:|||:| |:|:
Db        121 IKLAVYLISFFYYIYGMVYSLIST 144
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RESULT 7
YFR3_CAEEL
ID   YFR3_CAEEL     STANDARD;      PRT;   145 AA.
AC   Q22361;
DT   30-MAY-2000 (Rel. 39, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical 16.8 kDa protein T09E8.3 in chromosome V.
GN   T09E8.3.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Steward C.;
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   REVISIONS.
RA   Durbin R.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z78065; CAB01516.2; -.
DR   PIR; T24750; T24750.
DR   WormPep; T09E8.3; CE23961.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM      5     25       POTENTIAL.
FT   TRANSMEM     57     77       POTENTIAL.
FT   TRANSMEM    116    136       POTENTIAL.
SQ   SEQUENCE   145 AA;  16830 MW;  5C1C032B25DCE73C CRC64;

  Query Match             60.2%;  Score 472;  DB 1;  Length 145;
  Best Local Similarity   59.0%;  Pred. No. 1.4e-38;
  Matches   85;  Conservative   24;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              |||||||||||:|||:     |||||: :|  |||:|||||||:||  || |:||||:||
Db          1 MAFTFAAFCYLLALIAVGFCIFFAIYTVICVDELRTDYKNPIEQCRNLNQLILPEYIIHG 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              | |:|: : : :::  |:||  |||: |  ||||||||:||||||:|   |:   :  |
Db         61 TFTVLFIFSWQLISILANLPLAFYHIYTYAKRPVMSGPGIYDPTTILNRSTLSSTLRISW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||::||||||  ||| ||:|
Db        121 IKLAFYLVSFFYYLYAMIYTLVTS 144


RESULT 8
H163_HUMAN
ID   H163_HUMAN     STANDARD;      PRT;   139 AA.
AC   Q9P003;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Protein HSPC163.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=20499367; PubMed=11042152;
RA   Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA   Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA   Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT   "Cloning and functional analysis of cDNAs with open reading frames for
RT   300 previously undefined genes expressed in CD34+ hematopoietic
RT   stem/progenitor cells.";
RL   Genome Res. 10:1546-1560(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF161512; AAF29127.1; -.
DR   EMBL; BC000573; AAH00573.1; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
KW   Transmembrane.
FT   TRANSMEM      5     25       POTENTIAL.
FT   TRANSMEM     57     77       POTENTIAL.
FT   TRANSMEM    118    138       POTENTIAL.
SQ   SEQUENCE   139 AA;  16093 MW;  9452E9BDEC2A8DEF CRC64;

  Query Match             31.2%;  Score 244.5;  DB 1;  Length 139;
  Best Local Similarity   38.0%;  Pred. No. 9e-17;
  Matches   52;  Conservative   24;  Mismatches   60;  Indels    1;  Gaps    1;

Qy          7 AFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |  :: :||   |||| ::: ||   :|: || |    |: ||  |:|| : |    |:
Db          3 AVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTVLL 62

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
              | :  |    ||:|:  ::|:||:  |     |::||| | |   |    ||   || |:
Db         63 LMSLHWFIFLLNLPVATWNIYRYIMVP-SGNMGVFDPTEIHNRGQLKSHMKEAMIKLGFH 121

Qy        127 LLAFFYYLYGMIYVLVS 143
              || || ||| ||  |::
Db        122 LLCFFMYLYSMILALIN 138
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RESULT 9
ERV4_YEAST
ID   ERV4_YEAST     STANDARD;      PRT;   137 AA.
AC   P53173;
DT   01-OCT-1996 (Rel. 34, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   ER-derived vesicles protein ERV14.
GN   ERV14 OR YGL054C.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=97377993; PubMed=9234674;
RA   Feuermann M., de Montigny J., Potier S., Souciet J.-L.;
RT   "The characterization of two new clusters of duplicated genes
RT   suggests a 'Lego' organization of the yeast Saccharomyces cerevisiae
RT   chromosomes.";
RL   Yeast 13:861-869(1997).
RN   [2]
RP   SEQUENCE OF 1-18, AND FUNCTION.
RX   MEDLINE=98402530; PubMed=9732282;
RA   Powers J., Barlowe C.;
RT   "Transport of axl2p depends on erv14p, an ER-vesicle protein related
RT   to the Drosophila cornichon gene product.";
RL   J. Cell Biol. 142:1209-1222(1998).
CC   -!- FUNCTION: COULD REGULATE EXPORT OF THE BUD SITE AND AXIAL GROWTH
CC       SITES SELECTION PROTEIN AXL2 AND POSSIBLY OTHER SECRETORY
CC       PROTEINS FROM THE ENDOPLASMIC RETICULUM IN COPII-COATED VESICLES.
CC       SEEMS TO BE REQUIRED FOR AXIAL BUDDING PATTERN IN HAPLOID CELLS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. RESIDES IN THE
CC       ENDOPLASMIC AND GOLGI COMPARTMENTS, AND THEN PACKAGED INTO
CC       ENDOPLASMIC RETICULUM DERIVED VESICLES.
CC   -!- MISCELLANEOUS: DELETION OF ERV14 PRODUCES DEFECTS IN YEAST CELL
CC       POLARITY. STRAINS HOMOZYGOUS FOR ERV14 DELETION DO NOT SPORULATE.
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
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CC   ---------------------------------------------------------------------
DR   EMBL; Z72576; CAA96756.1; -.
DR   PIR; S64058; S64058.
DR   SGD; S0003022; ERV14.
DR   GO; GO:0030138; C:COPII-coated vesicle; IDA.
DR   GO; GO:0005789; C:endoplasmic reticulum membrane; IDA.
DR   GO; GO:0007120; P:axial budding; IMP.
DR   GO; GO:0006888; P:ER to Golgi transport; IMP.
DR   GO; GO:0007151; P:sporulation (sensu Saccharomyces); IMP.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Endoplasmic reticulum; Transmembrane; Golgi stack.
FT   INIT_MET      0      0
FT   DOMAIN        1      5       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM      6     26       POTENTIAL.
FT   DOMAIN       27     51       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     52     72       POTENTIAL.
FT   DOMAIN       73    110       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    111    131       POTENTIAL.
FT   DOMAIN      132    137       EXTRACELLULAR (POTENTIAL).
SQ   SEQUENCE   137 AA;  15799 MW;  C90D4BDC2550CDC0 CRC64;

  Query Match             27.1%;  Score 212.5;  DB 1;  Length 137;
  Best Local Similarity   32.8%;  Pred. No. 1.1e-13;
  Matches   45;  Conservative   31;  Mismatches   54;  Indels    7;  Gaps    2;

Qy          7 AFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |: ::||:::   :|  :   | : :|: || |||: |: :| |: ||  :|    ::|
Db          2 AWLFILAVVVNCINLFGQVHFTILYADLEADYINPIELCSKVNKLITPEAALHGALSLLF 61

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
              |    |    ||:|:|||::     : :     | | | |     |   ::| : || |:
Db         62 LLNGYWFVFLLNLPVLAYNL-----NKIYNKVQLLDATEIFRT--LGKHKRESFLKLGFH 114

Qy        127 LLAFFYYLYGMIYVLVS 143
               || ||:||| ||  |::
Db        115 LLMFFFYLYRMIMALIA 131


RESULT 10
YEY5_SCHPO
ID   YEY5_SCHPO     STANDARD;      PRT;   134 AA.
AC   O14038;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Hypothetical protein C2C4.05 in chromosome I.
GN   SPAC2C4.05.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z99259; CAB16365.1; -.
DR   PIR; T38516; T38516.
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DR   GeneDB_SPombe; SPAC2C4.05; -.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM      8     28       POTENTIAL.
FT   TRANSMEM     54     74       POTENTIAL.
FT   TRANSMEM    113    133       POTENTIAL.
SQ   SEQUENCE   134 AA;  15738 MW;  71E58F624E87F523 CRC64;

  Query Match             26.1%;  Score 204.5;  DB 1;  Length 134;
  Best Local Similarity   35.0%;  Pred. No. 6e-13;
  Matches   48;  Conservative   30;  Mismatches   52;  Indels    7;  Gaps    3;

Qy          6 AAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVM 65
              :|: |  :|:|| | |   ::  : : :|| |: ||||    || ||||    ||  ::
Db          3 SAWIYFTSLMLTCANIMLQMYFTVMYSDLKDDFINPIDLSRKLNWYVLPEMGFQAFSALL 62

Qy         66 FLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAF 125
               | :  |:|  ||:|:||::     :: :||   ::| |||   |: :  ||  : |||
Db         63 LLLSGAWITFLLNVPMLAWN-----AKMIMSNTHMHDSTTIFK-DVSSR-QKRSFFKLAC 115

Qy        126 YLLAFFYYLYGMIYVLV 142
             : : || ||:  :  ||
Db        116 FAVFFFVYLFLFVSRLV 132


RESULT 11
YB60_YEAST
ID   YB60_YEAST     STANDARD;      PRT;   142 AA.
AC   P38312;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical 16.3 kDa protein in DUR1,2-AME1 intergenic region.
GN   YBR210W OR YBR1457.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RA   Rieger M.;
RL   Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE CORNICHON FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z36079; CAA85174.1; -.
DR   PIR; S46084; S46084.
DR   SGD; S0000414; YBR210W.
DR   InterPro; IPR003377; Cornichon.
DR   Pfam; PF03311; Cornichon; 1.
DR   PROSITE; PS01340; CORNICHON; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM      8     28       POTENTIAL.
FT   TRANSMEM     56     76       POTENTIAL.
FT   TRANSMEM    115    135       POTENTIAL.
SQ   SEQUENCE   142 AA;  16347 MW;  E3329C122326A6A0 CRC64;

  Query Match             24.7%;  Score 193.5;  DB 1;  Length 142;
  Best Local Similarity   32.4%;  Pred. No. 7.3e-12;
  Matches   45;  Conservative   27;  Mismatches   52;  Indels   15;  Gaps    3;

Qy         10 YMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCA 69
               ::  |:|        |:  | : :|: || | |: |  :| | :|| :: ||   :||
Db          9 FVTGLILNCLNSICQIYFTILYGDLEADYINSIELCKRVNRLSVPEAILQAFISALFLFN 68

Qy         70 AEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNA-DI---LAYCQKEGWCKLAF 125
                 |    ||:|:|||:  :           :|  | :::| ||   |  |: | : || |
Db         69 GYWFVFLLNVPVLAYNASK----------VYKKTHLLDATDIFRKLGRCKIECFLKLGF 117

Qy        126 YLLAFFYYLYGMIYVLVSS 144
             ||| ||:| | |:  |: :
Db        118 YLLIFFPYFYRMVTALLEN 136


RESULT 12
TATC_HAEIN
ID   TATC_HAEIN     STANDARD;      PRT;   256 AA.
AC   P44560;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Sec-independent protein translocase protein tatC.
GN   TATC OR HI0188.
OS   Haemophilus influenzae.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC   Pasteurellaceae; Haemophilus.
OX   NCBI_TaxID=727;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Rd / KW20 / ATCC 51907;
RX   MEDLINE=95350630; PubMed=7542800;
RA   Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA   Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA   McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA   Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA   Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA   Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA   Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA   Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA   Venter J.C.;
RT   "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT   Rd.";
RL   Science 269:496-512(1995).
CC   -!- FUNCTION: REQUIRED FOR CORRECT LOCALIZATION OF PRECURSOR PROTEINS
CC       BEARING SIGNAL PEPTIDES WITH THE TWIN ARGININE CONSERVED MOTIF
CC       S/T-R-R-X-F-L-K. THIS SEC-INDEPENDENT PATHWAY IS TERMED TAT FOR
CC       TWIN-ARGININE TRANSLOCATION SYSTEM. THIS SYSTEM MAINLY TRANSPORTS
CC       PROTEINS WITH BOUND COFACTORS THAT REQUIRE FOLDING PRIOR TO EXPORT
CC       (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC       (Probable).
CC   -!- SIMILARITY: BELONGS TO THE TATC FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U32704; AAC21857.1; -.
DR   PIR; C64145; C64145.
DR   TIGR; HI0188; -.
DR   InterPro; IPR002033; Translocase.
DR   Pfam; PF00902; TatC; 1.
DR   TIGRFAMs; TIGR00945; tatC; 1.
DR   PROSITE; PS01218; TATC; 1.
KW   Transport; Protein transport; Translocation; Transmembrane;
KW   Inner membrane; Complete proteome.
FT   TRANSMEM     26     46       POTENTIAL.
FT   TRANSMEM     77     97       POTENTIAL.
FT   TRANSMEM    117    137       POTENTIAL.
FT   TRANSMEM    158    178       POTENTIAL.
FT   TRANSMEM    195    215       POTENTIAL.
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FT   TRANSMEM    217    237       POTENTIAL.
SQ   SEQUENCE   256 AA;  28734 MW;  F69971A264928DCC CRC64;

  Query Match             10.8%;  Score 84.5;  DB 1;  Length 256;
  Best Local Similarity   22.2%;  Pred. No. 0.37;
  Matches   32;  Conservative   28;  Mismatches   45;  Indels   39;  Gaps    7;

Qy          9 CYMLALLLTAALIFFA--IWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |  :  :|:  ||::|:  |:| :|           |:          ::   :   ||  :
Db         24 CVICVVLVFVALVYFSNDIYHFVA---------APLTAVMPKGATMIATNIQTPFFTPIK 74

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDP------TTIMNADILAYCQKEGW 120
              | |   : : :::| | | || :::      | ||          : :: || ||
Db         75 LTAI--VAIFISVPYLLYQIWAFIA------PALYQHEKRMIYPLLFSSTILFYCG---- 122

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
                 :|| ||:   :: || |
Db        123 -------VAFAYYI---VFPLVFS 136


RESULT 13
YGN9_YEAST
ID   YGN9_YEAST     STANDARD;      PRT;   802 AA.
AC   P53121;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Hypothetical 90.8 kDa protein in HUL5-SEC27 intergenic region.
GN   YGL139W OR G2812.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE OF 1-749 FROM N.A.
RC   STRAIN=S288C / FY1769;
RX   MEDLINE=97197983; PubMed=9046099;
RA   Voet M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert G.;
RT   "The sequence of a nearly unclonable 22.8 kb segment on the left arm
RT   chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A,
RT   TIP1, MRF1 genes and six new open reading frames.";
RL   Yeast 13:177-182(1997).
RN   [2]
RP   SEQUENCE OF 616-802 FROM N.A.
RC   STRAIN=S288c / FY1679;
RX   MEDLINE=96437978; PubMed=8840506;
RA   Escribano V., Eraso P., Portillo F., Mazon M.J.;
RT   "Sequence analysis of a 14.6 kb DNA fragment of Saccharomyces
RT   cerevisiae chromosome VII reveals SEC27, SSM1b, a putative
RT   S-adenosylmethionine-dependent enzyme and six new open reading
RT   frames.";
RL   Yeast 12:887-892(1996).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: TO YEAST YAL053W AND S.POMBE SPAC1F7.03.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X99960; CAA68223.1; -.
DR   EMBL; Z72661; CAA96851.1; -.
DR   EMBL; Z72660; CAA96850.1; -.
DR   EMBL; X92670; CAA63357.1; -.
DR   PIR; S64153; S64153.
DR   SGD; S0003107; YGL139W.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM      3     23       POTENTIAL.
FT   TRANSMEM    170    190       POTENTIAL.
FT   TRANSMEM    324    344       POTENTIAL.
FT   TRANSMEM    406    426       POTENTIAL.
FT   TRANSMEM    468    488       POTENTIAL.
FT   TRANSMEM    496    516       POTENTIAL.
FT   TRANSMEM    526    546       POTENTIAL.
FT   TRANSMEM    558    578       POTENTIAL.
SQ   SEQUENCE   802 AA;  90761 MW;  7BA13714AD912295 CRC64;

  Query Match             10.5%;  Score 82.5;  DB 1;  Length 802;
  Best Local Similarity   21.8%;  Pred. No. 1.8;
  Matches   29;  Conservative   19;  Mismatches   48;  Indels   37;  Gaps    5;

Qy         12 LALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVL---PEYLIH--AFFCVMF 66
              | :||:  |: :| |  : |           |          ||  |    ||::|   ||  ||
Db        412 LFILLSCGLMLWAAWRTVFFARRSVALYN--------NPAALLYGDEYVLHKYGFFYTMF 463

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
                    |     |: ||:|                                : : :: : |  |  :: |
Db        464 NANHYW----WNIVLLSY-------------------IFVKSLLVGFAQASGQTQVLFM 499

Qy        127 LLAFFYYLYGMIY 139
                :   :|   :||
Db        500 FILDLFYFVAIIY 512


RESULT 14
NU4M_CERCA
ID   NU4M_CERCA     STANDARD;      PRT;   446 AA.
AC   Q34048; Q34053;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   NADH-ubiquinone oxidoreductase chain 4 (EC 1.6.5.3).
GN   ND4.
OS   Ceratitis capitata (Mediterranean fruit fly).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Tephritoidea; Tephritidae; Ceratitis.
OX   NCBI_TaxID=7213;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Guatemala laboratory colony, and Hawaii laboratory colony;
RX   MEDLINE=95261546; PubMed=7742977;
RA   Gasparich G.E., Sheppard W.S., Han H.Y., McPheron B.A., Steck G.J.;
RT   "Analysis of mitochondrial DNA and development of PCR-based
RT   diagnostic molecular markers for Mediterranean fruit fly (Ceratitis
RT   capitata) populations.";
RL   Insect Mol. Biol. 4:61-67(1995).
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U12925; AAA85797.1; -.
DR   EMBL; U12924; AAA85796.1; -.
DR   InterPro; IPR003918; NADHub_oxred4.
DR   InterPro; IPR001750; Oxidored_q1.
DR   InterPro; IPR000260; Oxidored_q5_N.
DR   Pfam; PF00361; oxidored_q1; 1.
DR   Pfam; PF01059; oxidored_q5_N; 1.
DR   PRINTS; PR01437; NUOXDRDTASE4.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ   SEQUENCE   446 AA;  50967 MW;  E9AAAC06796897FD CRC64;

  Query Match             10.3%;  Score 81;  DB 1;  Length 446;
  Best Local Similarity   27.5%;  Pred. No. 1.4;
  Matches   41;  Conservative   21;  Mismatches   35;  Indels   52;  Gaps   11;
```

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Qy          10 YMLALLLTAAL-IFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLC 68
               |:|    |  :| :   |:::          |||    |||:|  :|  |          || |
Db         142 YLLFYTLLVSLPLLVGIFYL---------YKN----CNTMNFYLLSNY--------MFNC 180

Qy          69 AAEWLTLGL----NMPLLAYHIW---RYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWC 121
                  :| : |     ||:   |:|    ::  || ||       ::: | |:
Db         181 NLLYLAMILAFLVKMPMFLVHLWLPKAHVEAPV-SG-------SMILAGIM--------L 224

Qy         122 KLAFY-LLAFFYYL------YGMIYVLVS 143
               ||  | ||| | :|      |  |:| :|
Db         225 KLGGYGLLAVFSFLQLIGLKYNYIWVSIS 253


RESULT 15
P2L2_MOUSE
ID   P2L2_MOUSE     STANDARD;      PRT;   621 AA.
AC   Q9JLG4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Polycystic kidney disease 2-like 2 protein (Polycystin-L2).
GN   PKD2L2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=20221369; PubMed=10756092;
RA   Guo L., Schreiber T.H., Weremowicz S., Morton C.C., Lee C., Zhou J.;
RT   "Identification and characterization of a novel polycystin family
RT   member, polycystin-L2, in mouse and human: sequence, expression,
RT   alternative splicing, and chromosomal localization.";
RL   Genomics 64:241-251(2000).
CC   -!- FUNCTION: May function as a subunit of a cation channel and play a
CC       role in fertilization.
CC   -!- TISSUE SPECIFICITY: Expressed only in testis and heart.
CC   -!- SIMILARITY: BELONGS TO THE POLYCYSTIN FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AF182033; AAF65621.1; -.
DR   MGD; MGI:1858231; Pkd2l2.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR000434; PKD_1.
DR   InterPro; IPR003915; PKD_2.
DR   Pfam; PF00520; ion_trans; 1.
DR   PRINTS; PR00500; POLYCYSTIN1.
DR   PRINTS; PR01433; POLYCYSTIN2.
KW   Ionic channel; Glycoprotein; Coiled coil; Transmembrane.
FT   DOMAIN        1     31       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM     32     52       POTENTIAL.
FT   DOMAIN       53    277       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    278    298       POTENTIAL.
FT   DOMAIN      299    314       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    315    335       POTENTIAL.
FT   DOMAIN      336    360       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    361    381       POTENTIAL.
FT   DOMAIN      382    406       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    407    427       POTENTIAL.
FT   DOMAIN      428    468       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    469    489       POTENTIAL.
FT   DOMAIN      490    621       CYTOPLASMIC (POTENTIAL).
FT   SITE        126    138       POLYCYSTIN MOTIF.
FT   DOMAIN      521    551       COILED COIL (POTENTIAL).
FT   CARBOHYD    115    115       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    138    138       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   621 AA;  73684 MW;  30430013DD6A7531 CRC64;

  Query Match             10.1%;  Score 79.5;  DB 1;  Length 621;
  Best Local Similarity   17.9%;  Pred. No. 2.7;
  Matches   33;  Conservative   31;  Mismatches   51;  Indels   69;  Gaps    7;

Qy           1 MAFTFAAFCYMLALLLTAALI----------FFAIWHI--------------------IA 30
               :| :| |:| | : ||   |:          | | |||                    |:
Db         329 LAVSFYAYCNMQSFLLLGQLLKNTDSYPDFYFLAYWHIYYNNVIAITIFFAWIKIFKFIS 388

Qy          31 FDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYM 90
               |:|  :   : : :|  :  :|         |  : |:  : :  ||
Db         389 FNETMSQLSSTLSRC--MKDIV-------GFAIMFFIIFSAYAQLGF------------- 426

Qy          91 SRPVMSGPGLYDPTTIMNADI-----------LAYCQKEGWCKLAFYLLAFFYYLYGMIY 139
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Db         427 ---LVFGSQVDDFSTFQNSIFAQFRIVLGDFNFAGIQQANWILGPIYFITFIFFVF---F 480

Qy         140 VLVS 143
               ||::
Db         481 VLLN 484


Search completed: September 11, 2003, 14:42:49
Job time : 30 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:40:00 ; Search time 33 Seconds
(without alignments)
184.629 Million cell updates/sec

Title: US-09-918-585A-322
Perfect score: 784
Sequence: 1 MAFTFAAFCYMLALLLTAAL.....FYLLAFFYYLYGMIYVLVSS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	784	100.0	144	2	US-08-950-168-1	Sequence 1, Appli
2	784	100.0	144	4	US-09-365-705-1	Sequence 1, Appli
3	784	100.0	144	4	US-09-702-705-327	Sequence 327, App
4	784	100.0	144	4	US-09-736-457-327	Sequence 327, App
5	784	100.0	145	4	US-09-257-179-63	Sequence 63, Appl
6	548	69.9	144	2	US-08-950-168-3	Sequence 3, Appli
7	548	69.9	144	4	US-09-365-705-3	Sequence 3, Appli
8	244.5	31.2	139	4	US-09-489-847-219	Sequence 219, App
9	244.5	31.2	155	4	US-09-489-847-374	Sequence 374, App
10	196	25.0	35	4	US-09-257-179-120	Sequence 120, App
11	173	22.1	30	4	US-09-257-179-119	Sequence 119, App
12	167	21.3	30	4	US-09-257-179-118	Sequence 118, App
13	84.5	10.8	163	3	US-09-053-197A-26	Sequence 26, Appl
14	84.5	10.8	163	4	US-09-085-761A-26	Sequence 26, Appl
15	84.5	10.8	2254	2	US-08-286-819A-28	Sequence 28, Appl
16	84.5	10.8	2254	3	US-08-980-357-28	Sequence 28, Appl
17	77.5	9.9	692	4	US-09-252-991A-23903	Sequence 23903, A
18	73.5	9.4	505	4	US-09-328-352-7155	Sequence 7155, Ap
19	72	9.2	251	4	US-09-191-468-72	Sequence 72, Appl
20	72	9.2	251	4	US-09-191-468-74	Sequence 74, Appl
21	72	9.2	251	4	US-09-191-468-76	Sequence 76, Appl
22	72	9.2	251	4	US-09-191-468-78	Sequence 78, Appl
23	72	9.2	251	4	US-09-191-468-80	Sequence 80, Appl
24	72	9.2	251	4	US-09-191-468-82	Sequence 82, Appl
25	72	9.2	251	4	US-09-191-468-84	Sequence 84, Appl
26	72	9.2	251	4	US-09-191-468-86	Sequence 86, Appl
27	72	9.2	797	2	US-08-700-013B-19	Sequence 19, Appl
28	72	9.2	797	2	US-08-700-013B-21	Sequence 21, Appl
29	72	9.2	797	3	US-09-182-728A-2	Sequence 2, Appli
30	72	9.2	797	4	US-09-191-468-120	Sequence 120, App
31	72	9.2	797	4	US-09-191-468-122	Sequence 122, App
32	72	9.2	797	4	US-09-191-468-124	Sequence 124, App
33	72	9.2	797	4	US-09-795-232-2	Sequence 2, Appli
34	72	9.2	799	2	US-08-700-013B-27	Sequence 27, Appl
35	71	9.1	578	4	US-09-740-041-4	Sequence 4, Appli
36	70	8.9	177	2	US-08-700-013B-11	Sequence 11, Appl
37	70	8.9	177	2	US-08-700-013B-13	Sequence 13, Appl
38	70	8.9	300	4	US-09-393-634-19	Sequence 19, Appl
39	69.5	8.9	307	4	US-09-393-634-53	Sequence 53, Appl
40	69.5	8.9	600	4	US-09-198-452A-397	Sequence 397, App
41	68.5	8.7	352	4	US-09-205-815B-42	Sequence 42, Appl
42	68	8.7	526	4	US-09-328-352-7475	Sequence 7475, Ap
43	67.5	8.6	542	1	US-08-246-583-3	Sequence 3, Appli
44	67.5	8.6	542	4	US-09-636-791A-5	Sequence 5, Appli
45	66.5	8.5	54	4	US-09-225-024-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-950-168-1
; Sequence 1, Application US/08950168
; Patent No. 5968744
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0401 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1318847
US-08-950-168-1

Query Match 100.0%; Score 784; DB 2; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.8e-79;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 2
US-09-365-705-1
; Sequence 1, Application US/09365705
; Patent No. 6348576
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; Corley, Neil C.
; Shah, Purvi
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/365,705
; FILING DATE: 02-Aug-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/950,168
; FILING DATE: 14-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0401 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADNOT04
; CLONE: 1318847
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-365-705-1

peptide

Query Match 100.0%; Score 784; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.8e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 3
US-09-702-705-327
; Sequence 327, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-327

Query Match 100.0%; Score 784; DB 4; Length 144;
Best Local Similarity 100.0%; Pred. No. 3.8e-79;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 4
US-09-736-457-327
; Sequence 327, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSEQ for Windows Version 3.0

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; SEQ ID NO 327
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-736-457-327

  Query Match             100.0%;  Score 784;  DB 4;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-79;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 5
US-09-257-179-63
; Sequence 63, Application US/09257179
; Patent No. 6410709
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 29 Human Secreted Proteins
;  FILE REFERENCE: PZ015P1
;  CURRENT APPLICATION NUMBER: US/09/257,179
;  CURRENT FILING DATE: 1999-02-25
;  EARLIER APPLICATION NUMBER: PCT/US98/17709
;  EARLIER FILING DATE: 1998-08-27
;  EARLIER APPLICATION NUMBER: 60/056,270
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,271
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,247
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,073
;  EARLIER FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
;   LENGTH: 145
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (145)
;   OTHER INFORMATION: Xaa equals stop translation
US-09-257-179-63

  Query Match             100.0%;  Score 784;  DB 4;  Length 145;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-79;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 6
US-08-950-168-3
; Sequence 3, Application US/08950168
; Patent No. 5968744
; GENERAL INFORMATION:
;   APPLICANT:  Hillman, Jennifer L.
;   APPLICANT:  Corley, Neil C.
;   APPLICANT:  Shah, Purvi
;   TITLE OF INVENTION:  HUMAN CORNICHON PROTEIN
;   NUMBER OF SEQUENCES:  3
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;     STREET:  3174 Porter Drive
;     CITY:  Palo Alto
;     STATE:  CA
;     COUNTRY:  USA
;     ZIP:  94304
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Diskette
;     COMPUTER:  IBM Compatible
;     OPERATING SYSTEM:  DOS
;     SOFTWARE:  FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/950,168
;     FILING DATE:  Herewith
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Billings, Lucy J.
;     REGISTRATION NUMBER:  36,749
;     REFERENCE/DOCKET NUMBER:  PF-0401 US
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  650-855-0555
;     TELEFAX:  650-845-4166
;     TELEX:
;  INFORMATION FOR SEQ ID NO:  3:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  144 amino acids
;     TYPE:  amino acid
;     STRANDEDNESS:  single
;     TOPOLOGY:  linear
;   IMMEDIATE SOURCE:
;     LIBRARY:  GenBank
;     CLONE:  886769
US-08-950-168-3

  Query Match             69.9%;  Score 548;  DB 2;  Length 144;
  Best Local Similarity   66.7%;  Pred. No. 4.3e-53;
  Matches   96;  Conservative   23;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||| | || |::||:  | |||||||:|:||||||||||||||||||:|||||||||:|
Db          1 MAFNFTAFTYIVALIGDAFLIFFAIFHVIAFDELKTDYKNPIDQCNSLNPLVLPEYLLHI 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
                 |  ::||   || :| :|:||:|||||||| :|||||||||||||::  | |    :|||
Db         61 FLNLLFLFCGEWFSLCINIPLIAYHIWRYKNRPVMSGPGLYDPTTVLKTDTLYRNMREGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||| ||::||||:|||:| |:|:
Db        121 IKLAVYLISFFYYIYGMVYSLIST 144


RESULT 7
US-09-365-705-3
; Sequence 3, Application US/09365705
; Patent No. 6348576
;   GENERAL INFORMATION:
;        APPLICANT: Hillman, Jennifer L.
;                   Corley, Neil C.
;                   Shah, Purvi
;        TITLE OF INVENTION: HUMAN CORNICHON PROTEIN
```

```
;       NUMBER OF SEQUENCES: 3
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Incyte Pharmaceuticals, Inc.
;            STREET: 3174 Porter Drive
;            CITY: Palo Alto
;            STATE: CA
;            COUNTRY: USA
;            ZIP: 94304
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: DOS
;            SOFTWARE: FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/365,705
;            FILING DATE: 02-Aug-1999
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/950,168
;            FILING DATE: 14-OCT-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Billings, Lucy J.
;            REGISTRATION NUMBER: 36,749
;            REFERENCE/DOCKET NUMBER: PF-0401 US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 650-855-0555
;            TELEFAX: 650-845-4166
;            TELEX: <Unknown>
;   INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 144 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       IMMEDIATE SOURCE:
;            LIBRARY: GenBank
;            CLONE: 886769
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-365-705-3

  Query Match             69.9%;  Score 548;  DB 4;  Length 144;
  Best Local Similarity   66.7%;  Pred. No. 4.3e-53;
  Matches   96;  Conservative   23;  Mismatches   25;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||| | || |::||:  | |||||:|:||||||||||||||||||:||||||||||:|
Db          1 MAFNFTAFTYIVALIGDAFLIFFAIFHVIAFDELKTDYKNPIDQCNSLNPLVLPEYLLHI 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
                |  ::||   || :| :|:||:|||||| :|||||||||||||::  | |    :|||
Db         61 FLNLLFLFCGEWFSLCINIPLIAYHIWRYKNRPVMSGPGLYDPTTVLKTDTLYRNMREGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
                ||| ||::||||:|||:| |:|:
Db        121 IKLAVYLISFFYYIYGMVYSLIST 144


RESULT 8
US-09-489-847-219
; Sequence 219, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 219
;   LENGTH: 139
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-847-219

  Query Match             31.2%;  Score 244.5;  DB 4;  Length 139;
  Best Local Similarity   38.0%;  Pred. No. 1.3e-19;
  Matches   52;  Conservative   24;  Mismatches   60;  Indels    1;  Gaps    1;

Qy          7 AFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |  :: :||   |||| ::: ||   :|: || |    |: ||  |:|| : |    |:
Db          3 AVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTVLL 62

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
              | :  |    ||:|:  ::|:||:  |      |::||| | |    |    ||  || |:
Db         63 LMSLHWFIFLLNLPVATWNIYRYIMVP-SGNMGVFDPTEIHNRGQLKSHMKEAMIKLGFH 121

Qy        127 LLAFFYYLYGMIYVLVS 143
              || || ||| ||  |::
Db        122 LLCFFMYLYSMILALIN 138


RESULT 9
US-09-489-847-374
; Sequence 374, Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al
;  TITLE OF INVENTION: 98 Human Secreted Proteins
;  FILE REFERENCE: PZ031P1
;  CURRENT APPLICATION NUMBER: US/09/489,847
;  CURRENT FILING DATE: 2000-01-24
;  EARLIER APPLICATION NUMBER: PCT/US99/17130
;  EARLIER FILING DATE: 1999-07-29
;  EARLIER APPLICATION NUMBER: 60/094,657
;  EARLIER FILING DATE: 1998-07-30
;  EARLIER APPLICATION NUMBER: 60/095,486
;  EARLIER FILING DATE: 1998-08-05
;  EARLIER APPLICATION NUMBER: 60/096,319
;  EARLIER FILING DATE: 1998-08-12
;  EARLIER APPLICATION NUMBER: 60/095,454
;  EARLIER FILING DATE: 1998-08-06
;  EARLIER APPLICATION NUMBER: 60/095,455
;  EARLIER FILING DATE: 1998-08-06
;  NUMBER OF SEQ ID NOS: 376
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 374
;   LENGTH: 155
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-489-847-374

  Query Match             31.2%;  Score 244.5;  DB 4;  Length 155;
  Best Local Similarity   38.0%;  Pred. No. 1.5e-19;
  Matches   52;  Conservative   24;  Mismatches   60;  Indels    1;  Gaps    1;

Qy          7 AFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |  :: :||   |||| ::: ||   :|: || |    |: ||  |:|| : |    |:
Db         19 AVVFVFSLLDCCALIFLSVYFIITLSDLECDYINARSCCSKLNKWVIPELIGHTIVTVLL 78

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
              | :  |    ||:|:  ::|:||:  |      |::||| | |    |    ||  || |:
Db         79 LMSLHWFIFLLNLPVATWNIYRYIMVP-SGNMGVFDPTEIHNRGQLKSHMKEAMIKLGFH 137

Qy        127 LLAFFYYLYGMIYVLVS 143
```

```
                  || || ||| ||  |::
Db        138 LLCFFMYLYSMILALIN 154


RESULT 10
US-09-257-179-120
; Sequence 120, Application US/09257179
; Patent No. 6410709
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 29 Human Secreted Proteins
;  FILE REFERENCE: PZ015P1
;  CURRENT APPLICATION NUMBER: US/09/257,179
;  CURRENT FILING DATE: 1999-02-25
;  EARLIER APPLICATION NUMBER: PCT/US98/17709
;  EARLIER FILING DATE: 1998-08-27
;  EARLIER APPLICATION NUMBER: 60/056,270
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,271
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,247
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,073
;  EARLIER FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 120
;   LENGTH: 35
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-257-179-120

  Query Match             25.0%;  Score 196;  DB 4;  Length 35;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-15;
  Matches   35;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              |||||||||||||||||||||||||||||||||||
Db          1 WHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 35


RESULT 11
US-09-257-179-119
; Sequence 119, Application US/09257179
; Patent No. 6410709
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 29 Human Secreted Proteins
;  FILE REFERENCE: PZ015P1
;  CURRENT APPLICATION NUMBER: US/09/257,179
;  CURRENT FILING DATE: 1999-02-25
;  EARLIER APPLICATION NUMBER: PCT/US98/17709
;  EARLIER FILING DATE: 1998-08-27
;  EARLIER APPLICATION NUMBER: 60/056,270
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,271
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,247
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,073
;  EARLIER FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-257-179-119

  Query Match             22.1%;  Score 173;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYM 90
              ||||||||||||||||||||||||||||||
Db          1 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYM 30


RESULT 12
US-09-257-179-118
; Sequence 118, Application US/09257179
; Patent No. 6410709
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 29 Human Secreted Proteins
;  FILE REFERENCE: PZ015P1
;  CURRENT APPLICATION NUMBER: US/09/257,179
;  CURRENT FILING DATE: 1999-02-25
;  EARLIER APPLICATION NUMBER: PCT/US98/17709
;  EARLIER FILING DATE: 1998-08-27
;  EARLIER APPLICATION NUMBER: 60/056,270
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,271
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,247
;  EARLIER FILING DATE: 1997-08-29
;  EARLIER APPLICATION NUMBER: 60/056,073
;  EARLIER FILING DATE: 1997-08-29
;  NUMBER OF SEQ ID NOS: 128
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
;   LENGTH: 30
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-257-179-118

  Query Match             21.3%;  Score 167;  DB 4;  Length 30;
  Best Local Similarity   100.0%;  Pred. No. 7.3e-12;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 SRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||
Db          1 SRPVMSGPGLYDPTTIMNADILAYCQKEGW 30


RESULT 13
US-09-053-197A-26
; Sequence 26, Application US/09053197A
; Patent No. 6022952
;  GENERAL INFORMATION:
;    APPLICANT:  Weiner, Joel H.
;    APPLICANT:  Turner, Raymond J.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR PROTEIN
;    TITLE OF INVENTION:  SECRETION
;    NUMBER OF SEQUENCES:  72
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/053,197A
;      FILING DATE:  01-APR-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  MacKnight, Kamrin T.
;      REGISTRATION NUMBER:  38,230
;      REFERENCE/DOCKET NUMBER:  UALB-03293
;    TELECOMMUNICATION INFORMATION:
```

```
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  163 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-09-053-197A-26

  Query Match             10.8%;  Score 84.5;  DB 3;  Length 163;
  Best Local Similarity   22.2%;  Pred. No. 0.076;
  Matches   32;  Conservative   28;  Mismatches   45;  Indels   39;  Gaps    7;

Qy          9 CYMLALLLTAALIFFA--IWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              | :  :|:  ||::|:  |:| :|          |:          ::   :   || :
Db         14 CVICVVLVFVALVYFSNDIYHFVA---------APLTAVMPKGATMIATNIQTPFFTPIK 64

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDP------TTIMNADILAYCQKEGW 120
              | |    : : :::| | | || :::       | ||           : :: || ||
Db         65 LTAI--VAIFISVPYLLYQIWAFIA------PALYQHEKRMIYPLLFSSTILFYCG---- 112

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
                  :|| ||:   :: || |
Db        113 -------VAFAYYI---VFPLVFS 126


RESULT 14
US-09-085-761A-26
; Sequence 26, Application US/09085761A
; Patent No. 6335178
;  GENERAL INFORMATION:
;    APPLICANT:  Weiner, Joel H.
;    APPLICANT:  Turner, Raymond J.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR PROTEIN
;    TITLE OF INVENTION:  SECRETION
;    NUMBER OF SEQUENCES:  77
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Medlen & Carroll, LLP
;      STREET:  220 Montgomery Street, Suite 2200
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  United States of America
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/085,761A
;      FILING DATE:  28-MAY-1998
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Carroll, Peter G.
;      REGISTRATION NUMBER:  32,837
;      REFERENCE/DOCKET NUMBER:  UALB-03356
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 705-8410
;      TELEFAX:  (415) 397-8338
;  INFORMATION FOR SEQ ID NO:  26:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  163 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  not relevant
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-09-085-761A-26

  Query Match             10.8%;  Score 84.5;  DB 4;  Length 163;
  Best Local Similarity   22.2%;  Pred. No. 0.076;
  Matches   32;  Conservative   28;  Mismatches   45;  Indels   39;  Gaps    7;

Qy          9 CYMLALLLTAALIFFA--IWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              | :  :|:  ||::|:  |:| :|          |:          ::   :   || :
Db         14 CVICVVLVFVALVYFSNDIYHFVA---------APLTAVMPKGATMIATNIQTPFFTPIK 64

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDP------TTIMNADILAYCQKEGW 120
              | |    : : :::| | | || :::       | ||           : :: || ||
Db         65 LTAI--VAIFISVPYLLYQIWAFIA------PALYQHEKRMIYPLLFSSTILFYCG---- 112

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
                  :|| ||:   :: || |
Db        113 -------VAFAYYI---VFPLVFS 126


RESULT 15
US-08-286-819A-28
; Sequence 28, Application US/08286819A
; Patent No. 5871910
;  GENERAL INFORMATION:
;    APPLICANT:  ARTHUR, MICHEL
;    APPLICANT:  DUKTA-MALEN, SYLVIE
;    APPLICANT:  MOLINAS, CATHERINE
;    APPLICANT:  COURVALIN, PATRICE
;    TITLE OF INVENTION:  POLYPEPTIDES IMPLICATED IN THE
;    TITLE OF INVENTION:  EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR
;    TITLE OF INVENTION:  IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
;    TITLE OF INVENTION:  THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
;    NUMBER OF SEQUENCES:  54
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
;      ADDRESSEE:  P.C.
;      STREET:  1755 S. Jefferson Davis Highway, Suite 400
;      CITY:  Arlington
;      STATE:  Virginia
;      COUNTRY:  U.S.A.
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/286,819A
;      FILING DATE:  05-AUG-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/174,682
;      FILING DATE:  28-DEC-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/917,146
;      FILING DATE:  10-AUG-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/FR/91/00855
;      FILING DATE:  29-OCT-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  FR 9013579
;      FILING DATE:  31-OCT-1990
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Oblon, No. 5871910man F.
;      REGISTRATION NUMBER:  24,618
;      REFERENCE/DOCKET NUMBER:  660-060-0 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 413-3000
;      TELEFAX:  (703) 413-2220
;      TELEX:  248855 OPAT UR
;  INFORMATION FOR SEQ ID NO:  28:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2254 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
```

```
;    MOLECULE TYPE:  protein
US-08-286-819A-28

  Query Match             10.8%;  Score 84.5;  DB 2;  Length 2254;
  Best Local Similarity   22.7%;  Pred. No. 1.9;
  Matches   22;  Conservative   16;  Mismatches   32;  Indels   27;  Gaps    3;

Qy         50 PLVLPEYLI-----------HAFFCVMFLCAAEWLTLGLNMPLLAYHIWRY--------- 89
              ||   | ||:           |  :|:       |:  |  :|     :|||
Db       1114 PLASPFYLVPFTERVGLNYEHRHYCL-------WMAGGRCIPCSFASLWRYGNDNRQRVG 1166

Qy         90 MSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
              : | : :   :|   || :  : : | :|  |:: ||
Db       1167 IQRQIRAFQSMYQCGTIRDFRLYSSCAEESRCEIYFY 1203


Search completed: September 11, 2003, 14:50:22
Job time : 34 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:36:10 ; Search time 40 Seconds
(without alignments)
346.207 Million cell updates/sec

Title: US-09-918-585A-322
Perfect score: 784
Sequence: 1 MAFTFAAFCYMLALLLTAAL.....FYLLAFFYYLYGMIYVLVSS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	548	69.9	144	2	A56724	cni protein - frui
2	472	60.2	145	2	T24750	hypothetical prote
3	443	56.5	136	2	A89261	protein T09E8.3 [i
4	212.5	27.1	138	2	S64058	probable membrane
5	204.5	26.1	134	2	T38516	cornichon homolog
6	193.5	24.7	142	2	S46084	probable membrane
7	159.5	20.3	126	2	D96653	hypothetical prote
8	128	16.3	160	2	G90096	hypothetical prote
9	128	16.3	160	2	H90129	hypothetical prote
10	128	16.3	160	2	B90133	hypothetical prote
11	122.5	15.6	145	2	T06616	hypothetical prote
12	90	11.5	249	2	T50162	hypothetical prote
13	86	11.0	259	2	AG0915	sec-independent pr
14	84.5	10.8	256	2	C64145	hypothetical prote
15	83.5	10.7	495	2	T20885	hypothetical prote
16	82.5	10.5	802	2	S64153	probable membrane
17	82	10.5	422	2	AB3635	probable O-antigen
18	81	10.3	502	1	I30010	NADH2 dehydrogenas
19	81	10.3	502	2	T27908	hypothetical prote
20	79.5	10.1	2848	2	T32550	hypothetical prote
21	77.5	9.9	296	2	H69796	lactose permease h
22	77.5	9.9	661	2	G82985	probable choline t
23	77	9.8	270	2	F95978	probable sugar upt
24	77	9.8	270	2	C75473	probable Sec-indep
25	76.5	9.8	354	2	T22967	hypothetical prote
26	76.5	9.8	382	2	D58930	ubiquinol-cytochro
27	76	9.7	559	2	B72487	hypothetical prote
28	76	9.7	590	1	S34960	NADH2 dehydrogenas
29	75.5	9.6	209	1	S48459	probable dual spec
30	75.5	9.6	498	2	A97710	aDP,ATP carrier pr
31	75	9.6	484	2	T26190	hypothetical prote
32	74.5	9.5	292	2	AC1460	sugar ABC transpor
33	74.5	9.5	292	2	AD1097	sugar ABC transpor
34	74.5	9.5	323	2	F84526	hypothetical prote
35	74.5	9.5	458	2	S61974	SSU1 protein - yea
36	74	9.4	253	2	A83719	hypothetical prote
37	73	9.3	154	2	S30728	hypothetical prote
38	73	9.3	258	2	H65188	sec-independent pr
39	73	9.3	258	2	H91224	Sec-independent pr
40	73	9.3	258	2	F86071	sec-independent pr
41	73	9.3	363	1	CBUTB	ubiquinol-cytochro
42	73	9.3	420	2	T32157	hypothetical prote
43	73	9.3	497	2	AG1768	hypothetical prote
44	73	9.3	1242	2	T39453	probable mrna stab
45	72.5	9.2	164	2	B81414	probable integral

ALIGNMENTS

RESULT 1
A56724
cni protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 21-Jul-2000
C;Accession: A56724
R;Roth, S.; Neuman-Silberberg, F.S.; Barcelo, G.; Schuepbach, T.
Cell 81, 967-978, 1995
A;Title: cornichon and the EGF receptor signaling process are necessary for both anterio
A;Reference number: A56724; MUID:95300228; PMID:7540118
A;Accession: A56724
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-144 <ROT>
A;Cross-references: GB:U28069; NID:g886768; PIDN:AAA86527.1; PID:g886769
C;Genetics:
A;Gene: FlyBase:cni
A;Cross-references: FlyBase:FBgn0000339
C;Superfamily: Drosophila cornichon protein

Query Match 69.9%; Score 548; DB 2; Length 144;
Best Local Similarity 66.7%; Pred. No. 9e-50;
Matches 96; Conservative 23; Mismatches 25; Indels 0; Gaps 0;

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Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||| | || |::||:  | ||||||:|:|||||||||||||||||:||||||||||:|
Db          1 MAFNFTAFTYIVALIGDAFLIFFAIFHVIAFDELKTDYKNPIDQCNSLNPLVLPEYLLHI 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              |  ::||   || :| :|:||:|||||| :|||||||||||||::  | |    :|||
Db         61 FLNLLFLFCGEWFSLCINIPLIAYHIWRYKNRPVMSGPGLYDPTTVLKTDTLYRNMREGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||| ||::||||:|||:| |:|:
Db        121 IKLAVYLISFFYYIYGMVYSLIST 144
```

RESULT 2
T24750
hypothetical protein T09E8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C;Accession: T24750
R;Steward, C.
submitted to the EMBL Data Library, August 1996
A;Reference number: Z19931
A;Accession: T24750
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-145 <WIL>
A;Cross-references: EMBL:Z78065; PIDN:CAB01516.2; GSPDB:GN00023; CESP:T09E8.3
A;Experimental source: clone T09E8

```
C;Genetics:
A;Gene: CESP:T09E8.3
A;Map position: 5
A;Introns: 27/3; 136/2
C;Superfamily: Drosophila cornichon protein

  Query Match             60.2%;  Score 472;  DB 2;  Length 145;
  Best Local Similarity   59.0%;  Pred. No. 7.3e-42;
  Matches   85;  Conservative   24;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||:|||:     |||||: :|  |||:|||||||:||  || |:||||:||
Db          1 MAFTFAAFCYLLALIAVGFCIFFAIYTVICVDELRTDYKNPIEQCRNLNQLILPEYIIHG 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              | |:|: : : :::  |:||  |||: |  ||||||||:||||||:|   |:   :  |
Db         61 TFTVLFIFSWQLISILANLPLAFYHIYTYAKRPVMSGPGIYDPTTILNRSTLSSTLRISW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||:|||||| ||| ||:|
Db        121 IKLAFYLVSFFYYLYAMIYTLVTS 144


RESULT 3
A89261
protein T09E8.3 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: A89261
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: A89261
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-136 <STO>
A;Cross-references: GB:chr_V; PIDN:CAB01516.1; PID:g3879700; GSPDB:GN00023; CESP:T09E8.3
C;Genetics:
A;Gene: T09E8.3
A;Map position: 5
C;Superfamily: Drosophila cornichon protein

  Query Match             56.5%;  Score 443;  DB 2;  Length 136;
  Best Local Similarity   58.5%;  Pred. No. 7.1e-39;
  Matches   79;  Conservative   23;  Mismatches   33;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||:|||:     |||||: :|  |||:|||||||:||  || |:||||:||
Db          1 MAFTFAAFCYLLALIAVGFCIFFAIYTVICVDELRTDYKNPIEQCRNLNQLILPEYIIHG 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              | |:|: : : :::  |:||  |||: |  ||||||||:||||||:|   |:   :  |
Db         61 TFTVLFIFSWQLISILANLPLAFYHIYTYAKRPVMSGPGIYDPTTILNRSTLSSTLRISW 120

Qy        121 CKLAFYLLAFFYYLY 135
              |||||||::||||||
Db        121 IKLAFYLVSFFYYLY 135


RESULT 4
S64058
probable membrane protein YGL054c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein G3474
C;Species: Saccharomyces cerevisiae
C;Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 19-Apr-2002
C;Accession: S64058
R;Feuermann, M.; Potier, S.; Souciet, J.L.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64044
A;Accession: S64058
A;Molecule type: DNA
A;Residues: 1-138 <FEU>
A;Cross-references: EMBL:Z72576; NID:g1322549; PID:g1322550; GSPDB:GN00007; MIPS:YGL054c
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:ERV14; MIPS:YGL054c
A;Cross-references: SGD:S0003022
A;Map position: 7L
C;Superfamily: Drosophila cornichon protein
C;Keywords: transmembrane protein
F;2-18/Domain: transmembrane #status predicted <TM1>
F;57-73/Domain: transmembrane #status predicted <TM2>
F;116-132/Domain: transmembrane #status predicted <TM3>

  Query Match             27.1%;  Score 212.5;  DB 2;  Length 138;
  Best Local Similarity   32.8%;  Pred. No. 6.8e-15;
  Matches   45;  Conservative   31;  Mismatches   54;  Indels    7;  Gaps    2;

Qy          7 AFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              |: ::||:::    :|  :   | : :|: || |||: |: :| |: ||  :|    ::|
Db          3 AWLFILAVVVNCINLFGQVHFTILYADLEADYINPIELCSKVNKLITPEAALHGALSLLF 62

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFY 126
              |    |    ||:|:|||::       : :   | | | |     |  ::| : || |:
Db         63 LLNGYWFVFLLNLPVLAYNL-----NKIYNKVQLLDATEIFRT--LGKHKRESFLKLGFH 115

Qy        127 LLAFFYYLYGMIYVLVS 143
              || ||:||| ||  |::
Db        116 LLMFFFYLYRMIMALIA 132


RESULT 5
T38516
cornichon homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C;Accession: T38516
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z21748
A;Accession: T38516
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-134 <OLI>
A;Cross-references: EMBL:Z99259; PIDN:CAB16365.1; GSPDB:GN00066; SPDB:SPAC2C4.05
A;Experimental source: strain 972h-; cosmid c2C4
C;Genetics:
A;Gene: SPDB:SPAC2C4.05
A;Map position: 1
A;Introns: 41/1
C;Superfamily: Drosophila cornichon protein

  Query Match             26.1%;  Score 204.5;  DB 2;  Length 134;
  Best Local Similarity   35.0%;  Pred. No. 4.5e-14;
  Matches   48;  Conservative   30;  Mismatches   52;  Indels    7;  Gaps    3;

Qy          6 AAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVM 65
              :|: |  :|:|| | |    ::  : : :|| |: ||||    ||  ||||    ||  ::
Db          3 SAWIYFTSLMLTCANIMLQMYFTVMYSDLKDDFINPIDLSRKLNWYVLPEMGFQAFSALL 62

Qy         66 FLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAF 125
              | :  |:|  ||:|:||::     :: :||   ::| |||    |: :  ||  : |||
Db         63 LLLSGAWITFLLNVPMLAWN-----AKMIMSNTHMHDSTTIFK-DVSSR-QKRSFFKLAC 115

Qy        126 YLLAFFYYLYGMIYVLV 142
              : : || ||:  :  ||
Db        116 FAVFFFVYLFLFVSRLV 132


RESULT 6
S46084
probable membrane protein YBR210w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBR1457
```

```
C;Species: Saccharomyces cerevisiae
C;Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 19-Apr-2002
C;Accession: S46084
R;Rieger, M.
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45734
A;Accession: S46084
A;Molecule type: DNA
A;Residues: 1-142 <RIE>
A;Cross-references: EMBL:Z36079; NID:g536591; PID:g536592; GSPDB:GN00002; MIPS:YBR210w
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YBR210w
A;Cross-references: SGD:S0000414
A;Map position: 2R
C;Superfamily: Drosophila cornichon protein
C;Keywords: transmembrane protein
F;5-22/Domain: transmembrane #status predicted <TM1>
F;59-76/Domain: transmembrane #status predicted <TM2>
F;107-127/Domain: transmembrane #status predicted <TM3>

  Query Match             24.7%;  Score 193.5;  DB 2;  Length 142;
  Best Local Similarity   32.4%;  Pred. No. 6.7e-13;
  Matches   45;  Conservative   27;  Mismatches   52;  Indels   15;  Gaps    3;

Qy         10 YMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCA 69
              ::  |:|        |:  | : :|: || | |: |  :| | :|| :: ||   :||
Db          9 FVTGLILNCLNSICQIYFTILYGDLEADYINSIELCKRVNRLSVPEAILQAFISALFLFN 68

Qy         70 AEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNA-DI---LAYCQKEGWCKLAF 125
              |    ||:|:|||:  :           :|  | :::| ||    |  |: | : || |
Db         69 GYWFVFLLNVPVLAYNASK----------VYKKTHLLDATDIFRKLGRCKIECFLKLGF 117

Qy        126 YLLAFFYYLYGMIYVLVSS 144
             ||| ||:| | |:  |: :
Db        118 YLLIFFFYFYRMVTALLEN 136


RESULT 7
D96653
hypothetical protein F16P17.3 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: D96653
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D96653
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-126 <STO>
A;Cross-references: GB:AE005173; NID:g8493595; PIDN:AAF75818.1; GSPDB:GN00141
C;Genetics:
A;Gene: F16P17.3
A;Map position: 1
C;Superfamily: Drosophila cornichon protein

  Query Match             20.3%;  Score 159.5;  DB 2;  Length 126;
  Best Local Similarity   28.6%;  Pred. No. 2e-09;
  Matches   36;  Conservative   29;  Mismatches   54;  Indels    7;  Gaps    2;

Qy         10 YMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCA 69
              :::: |:   |:   :: :|:  :|: || || |  : :| :|||| ::  | || :|
Db          7 WIISFLILITLLGLIVYQLISLADLEFDYINPYDSASRINFVVLPESILQGFLCVFYLVT 66

Qy         70 AEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLA 129
              |    | :| | |:   |  :       | | | | |  :| : :|:   |||: :|
Db         67 GHWFMALLCVPYLYYNFHLYSRK-----QHLIDVTEIFN--LLDWEKKKRLFKLAYIILT 119

Qy        130 FFYYLY 135
              |  ::
Db        120 LFLTIF 125


RESULT 8
G90096
hypothetical protein orf160 [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: G90096
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: G90096
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <DOU>
A;Cross-references: GB:AF165818; NID:g13794527; PIDN:AAK39902.1; GSPDB:GN00150
C;Genetics:
A;Gene: orf160
A;Map position: 1
A;Genome: nucleomorph
C;Keywords: nucleomorph

  Query Match             16.3%;  Score 128;  DB 2;  Length 160;
  Best Local Similarity   29.4%;  Pred. No. 4.9e-06;
  Matches   32;  Conservative   22;  Mismatches   47;  Indels    8;  Gaps    3;

Qy         33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSR 92
              :| ||  ||:: |: :| | :|||| | |  : |:    |:   || | : |:  ::
Db         38 DLSTDTVNPVEVCDKVNQLKVPEYLAHLFLSIAFVIRGWWIVGFLNFPPIFYNFAQW--- 94

Qy         93 PVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLY-GMIYV 140
              |   |  | | :|:   :    | ||::   | ::  ||:|
Db         95 --YEGKHQLDSAQIFN--VLSRELRVIKAKSAFFIIIVIYTIWEWMIWV 139


RESULT 9
H90129
hypothetical protein orf160 [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: H90129
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: H90129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <DOU>
A;Cross-references: GB:AF083031; NID:g13794404; PIDN:AAK39781.1; GSPDB:GN00152
C;Genetics:
A;Gene: orf160
A;Map position: 3
A;Genome: nucleomorph
C;Keywords: nucleomorph

  Query Match             16.3%;  Score 128;  DB 2;  Length 160;
  Best Local Similarity   29.4%;  Pred. No. 4.9e-06;
  Matches   32;  Conservative   22;  Mismatches   47;  Indels    8;  Gaps    3;

Qy         33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSR 92
              :| ||  ||:: |: :| | :|||| | |  : |:    |:   || | : |:  ::
Db         38 DLSTDTVNPVEVCDKVNQLKVPEYLAHLFLSIAFVIRGWWIVGFLNFPPIFYNFAQW--- 94
```

```
Qy          93 PVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLY-GMIYV 140
               |    |   | |  :|:   :    | ||:::   | ::  ||:|
Db          95 --YEGKHQLDSAQIFN--VLSRELRVIKAKSAFFIIIVIYTIWEWMIWV 139
```

RESULT 10
B90133
hypothetical protein orf160 [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: B90133
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
A;Accession: B90133
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-160 <DOU>
A;Cross-references: GB:AF083031; NID:g13794354; PIDN:AAK39731.1; GSPDB:GN00152
C;Genetics:
A;Gene: orf160
A;Map position: 3
A;Genome: nucleomorph
C;Keywords: nucleomorph

  Query Match 16.3%; Score 128; DB 2; Length 160;
  Best Local Similarity 29.4%; Pred. No. 4.9e-06;
  Matches 32; Conservative 22; Mismatches 47; Indels 8; Gaps 3;

```
Qy          33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSR 92
               :| ||  ||:: |: :| | :|||| | |  : |:    |:   || | : |:  ::
Db          38 DLSTDTVNPVEVCDKVNQLKVPEYLAHLFLSIAFVIRGWWIVGFLNFPFIFYNFAQW--- 94

Qy          93 PVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLY-GMIYV 140
               |    |   | |  :|:   :    | ||:::   | ::  ||:|
Db          95 --YEGKHQLDSAQIFN--VLSRELRVIKAKSAFFIIIVIYTIWEWMIWV 139
```

RESULT 11
T06616
hypothetical protein F16J13.160 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C;Accession: T06616
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft,
submitted to the Protein Sequence Database, April 1999
A;Reference number: Z15789
A;Accession: T06616
A;Molecule type: DNA
A;Residues: 1-145 <BEV>
A;Cross-references: EMBL:AL049638; GSPDB:GN00062; ATSP:F16J13.160
A;Experimental source: cultivar Columbia; BAC clone F16J13
C;Genetics:
A;Gene: ATSP:F16J13.160
A;Map position: 4
A;Introns: 34/3; 95/2; 136/2

  Query Match 15.6%; Score 122.5; DB 2; Length 145;
  Best Local Similarity 29.0%; Pred. No. 1.7e-05;
  Matches 31; Conservative 21; Mismatches 48; Indels 7; Gaps 2;

```
Qy          33 ELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSR 92
               :|: |  || |  : :| :|||| : |: ::   |   |::| | |:|  || |
Db          40 DLEFDRINPYDVSSRINRMVLPEFGLQGLLCLYYILTGHWFMAVLSLPHLFYNIRLYMKR 99

Qy          93 PVMSGPGLYDPTTIMNADILAYCQKEGWCKLAFYLLAFFYYLYGMIY 139
                  | | : | :   : ||:   |:   |: |   | :|:
Db         100 -----EHLADVTELYNTN--KWEQKKRVYKIGHIALSIFITTYWLIH 139
```

RESULT 12
T50162
hypothetical protein SPAC227.06 [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C;Accession: T50162
R;Zimmermann, W.; Wambutt, R.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, November 1999
A;Reference number: Z25036
A;Accession: T50162
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-249 <ZIM>
A;Cross-references: EMBL:AL133156; PIDN:CAB61455.1; GSPDB:GN00066; SPDB:SPAC227.06
A;Experimental source: strain 972h(-); cosmid c227
C;Genetics:
A;Gene: SPDB:SPAC227.06
A;Map position: 1

  Query Match 11.5%; Score 90; DB 2; Length 249;
  Best Local Similarity 22.1%; Pred. No. 0.068;
  Matches 33; Conservative 26; Mismatches 50; Indels 40; Gaps 6;

```
Qy          10 YMLALLLTAALIFFA--------IWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAF 61
               | :  |::|| | :          :| |: :               |  || :|    :: :
Db         122 YSIKKLISAASIIYGYTTIIAVLLWGILVW-------------NKCNPKLLDCLCLYGY 167

Qy          62 FCVMFLCAAEWLTLGLNMP------LLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYC 115
                 ::      || : |  |        || || :|    |:: | ||       :  ::   |
Db         168 ANIV------WLPVSLATPPFGLLSTLASHIVKY----VLTGIGLLISIVFLTRNLYPIC 217

Qy         116 QKEG--WCKLAFYLLAFFYYLYGMIYVLV 142
               |: |   |||  : :  |: |  :   |:
Db         218 QQAGSNLCKLLLFGIIVFHCLLALSLQLI 246
```

RESULT 13
AG0915
sec-independent protein translocase protein [imported] - Salmonella enterica subsp. ente
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AG0915
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AG0915
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07917.1; PID:g16504462; GSPDB:GN00176
C;Genetics:
A;Gene: tatC
C;Superfamily: conserved hypothetical protein HI0188

  Query Match 11.0%; Score 86; DB 2; Length 259;
  Best Local Similarity 23.7%; Pred. No. 0.19;
  Matches 33; Conservative 25; Mismatches 35; Indels 46; Gaps 8;

```
Qy           9 CYMLALLLTAALIFFA--IWHIIAFDELK----------TDYKNPIDQCNTLNPLVLPEY 56
               | :  ||:  |||:||  |:|::|   :|           ||  :|       |: |
Db          23 CIVAVLLIFLALIYFANDIYHLVAAPLIKQMPQGATMIATDVASPF-----FTPIKL--- 74

Qy          57 LIHAFFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQ 116
                           |:     ::| |: |:: | :| :::      | ||      :   :|
Db          75 --------TFM-----VSLILSAPVILYQVWAFIA------PALYKHERRLVVPLLVS-- 113

Qy         117 KEGWCKLAFYL-LAFFYYL 134
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Db        114 ----SSLLFYIGMAFAYFV 128


RESULT 14
C64145
hypothetical protein HI0188 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Sep-1999
C;Accession: C64145
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64145
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-256 <TIGR>
A;Cross-references: GB:U32704; GB:L42023; NID:g1573143; PIDN:AAC21857.1; PID:g1573146; T
A;Note: best homolog was a hypothetical protein from Escherichia coli
C;Superfamily: conserved hypothetical protein HI0188

  Query Match             10.8%;  Score 84.5;  DB 2;  Length 256;
  Best Local Similarity   22.2%;  Pred. No. 0.26;
  Matches   32;  Conservative   28;  Mismatches   45;  Indels   39;  Gaps    7;

Qy          9 CYMLALLLTAALIFFA--IWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFFCVMF 66
              | :  :|:  ||::|:  |:| :|          |:         ::   :   ||  :
Db         24 CVICVVLVFVALVYFSNDIYHFVA---------APLTAVMPKGATMIATNIQTPFFTPIK 74

Qy         67 LCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDP------TTIMNADILAYCQKEGW 120
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Db         75 LTAI--VAIFISVPYLLYQIWAFIA------PALYQHEKRMIYPLLFSSTILFYCG---- 122

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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Db        123 -------VAFAYYI---VFPLVFS 136


RESULT 15
T20885
hypothetical protein F14D7.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20885
R;Berks, M.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19340
A;Accession: T20885
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-495 <WIL>
A;Cross-references: EMBL:Z77658; PIDN:CAB01157.1; GSPDB:GN00023; CESP:F14D7.6
A;Experimental source: clone F14D7
C;Genetics:
A;Gene: CESP:F14D7.6
A;Map position: 5
A;Introns: 20/1; 46/2; 90/3; 113/3; 142/1; 199/2; 218/2; 244/3; 301/1; 333/2; 451/2

  Query Match             10.7%;  Score 83.5;  DB 2;  Length 495;
  Best Local Similarity   25.0%;  Pred. No. 0.64;
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Qy          3 FTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEY-LIHAF 61
              ||  ||  ::|::  || :    :        | :|   ||:  : : :|:|:| |  |
Db        265 FTVVAF--LMAIVCLAACVIVQCF-------FKENYVGIIDKNESDSNVVIPKYDLAGAL 315

Qy         62 FCVMFLCAAE-----------WLTLGLNMPLLAYHIWRYMSRP--VMSGPGLYDPTTIM 107
                |:                : :||   || | :: |   |    |||  | |
Db        316 TCIYLFMIVNIIATNVEVDKRIQMLIGLGFFLL-YQVFMY---PWGFYSGPLDYLPDG-K 370

Qy        108 NADILAYC-QKEGWCK------LAFYLLAFFYYLYGMIYVLVSS 144
              : |:   | |   ||:      |  ||: |  : :|: :  | |
Db        371 DTDVAGGCYQSYKWCQWTTRVPLPVYLICFIVF-FGIAFPFVES 413


Search completed: September 11, 2003, 14:42:19
Job time : 47 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:41:46 ; Search time 61 Seconds
(without alignments)
344.449 Million cell updates/sec

Title: US-09-918-585A-322
Perfect score: 784
Sequence: 1 MAFTFAAFCYMLALLLTAAL.....FYLLAFFYYLYGMIYVLVSS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	784	100.0	144	10	US-09-978-295A-322	Sequence 322, App
2	784	100.0	144	10	US-09-736-457-327	Sequence 327, App
3	784	100.0	144	10	US-09-978-697-322	Sequence 322, App
4	784	100.0	144	10	US-09-902-941-327	Sequence 327, App
5	784	100.0	144	10	US-09-978-192A-322	Sequence 322, App
6	784	100.0	144	10	US-09-999-832A-322	Sequence 322, App
7	784	100.0	144	10	US-09-849-626-327	Sequence 327, App
8	784	100.0	144	11	US-09-978-189-322	Sequence 322, App
9	784	100.0	144	11	US-09-978-608A-322	Sequence 322, App
10	784	100.0	144	11	US-09-978-585A-322	Sequence 322, App
11	784	100.0	144	11	US-09-978-191A-322	Sequence 322, App
12	784	100.0	144	11	US-09-978-403A-322	Sequence 322, App
13	784	100.0	144	11	US-09-978-564A-322	Sequence 322, App
14	784	100.0	144	11	US-09-999-833A-322	Sequence 322, App
15	784	100.0	144	11	US-09-981-915A-322	Sequence 322, App
16	784	100.0	144	11	US-09-978-824-322	Sequence 322, App
17	784	100.0	144	11	US-09-918-585A-322	Sequence 322, App
18	784	100.0	144	11	US-09-978-423A-322	Sequence 322, App
19	784	100.0	144	11	US-09-978-193A-322	Sequence 322, App
20	784	100.0	144	11	US-09-999-830A-322	Sequence 322, App
21	784	100.0	144	11	US-09-978-757A-322	Sequence 322, App
22	784	100.0	144	11	US-09-978-187B-322	Sequence 322, App
23	784	100.0	144	11	US-09-978-643A-322	Sequence 322, App
24	784	100.0	144	11	US-09-476-300-327	Sequence 327, App
25	784	100.0	144	12	US-09-978-375A-322	Sequence 322, App
26	784	100.0	144	12	US-09-978-188A-322	Sequence 322, App
27	784	100.0	144	12	US-09-978-298A-322	Sequence 322, App
28	784	100.0	144	12	US-10-143-031A-322	Sequence 322, App
29	784	100.0	144	12	US-10-002-967A-322	Sequence 322, App
30	784	100.0	144	12	US-10-017-083A-322	Sequence 322, App
31	784	100.0	144	12	US-10-143-030A-322	Sequence 322, App
32	784	100.0	144	12	US-10-216-163-120	Sequence 120, App
33	784	100.0	144	12	US-10-145-128A-322	Sequence 322, App
34	784	100.0	144	14	US-10-044-477-1	Sequence 1, Appli
35	784	100.0	144	15	US-10-227-884-120	Sequence 120, App
36	784	100.0	144	15	US-10-230-163-120	Sequence 120, App
37	784	100.0	144	15	US-10-230-338-120	Sequence 120, App
38	784	100.0	144	15	US-10-218-631-120	Sequence 120, App
39	784	100.0	144	15	US-10-017-081A-322	Sequence 322, App
40	784	100.0	144	15	US-10-230-414-120	Sequence 120, App
41	784	100.0	144	15	US-10-017-754-327	Sequence 327, App
42	784	100.0	144	15	US-10-167-749-322	Sequence 322, App
43	784	100.0	144	15	US-10-013-921A-322	Sequence 322, App
44	784	100.0	144	15	US-10-216-159A-120	Sequence 120, App
45	784	100.0	144	15	US-10-013-929A-322	Sequence 322, App

ALIGNMENTS

RESULT 1
US-09-978-295A-322
; Sequence 322, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
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;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085323
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;  PRIOR FILING DATE: 1998-05-15
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;  PRIOR APPLICATION NUMBER: 60/085573
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;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

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Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 2
US-09-736-457-327
; Sequence 327, Application US/09736457
; Patent No. US20020168637A1
; GENERAL INFORMATION:
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  Lodes, Michael A.
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Vedvick, Tom
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Retter, Marc
;  APPLICANT:  Mannion, Jane
;  APPLICANT:  Fan, Liqun
;  APPLICANT:  Wang, Aijun
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE:  210121.478C15
;  CURRENT APPLICATION NUMBER: US/09/736,457
;  CURRENT FILING DATE:  2000-12-13
;  NUMBER OF SEQ ID NOS:  1864
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 327
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-736-457-327

  Query Match             100.0%;  Score 784;  DB 10;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-78;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 3
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; Sequence 322, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C27
;  CURRENT APPLICATION NUMBER: US/09/978,697
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 09/918585
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Query Match 100.0%; Score 784; DB 10; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
US-09-902-941-327
; Sequence 327, Application US/09902941
; Patent No. US20020172952A1
; GENERAL INFORMATION:
;  APPLICANT: Henderson, Robert A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Johnson, Jeffrey C.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Marnerakis, Margarita
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Bangur, Chaitanya S.
;  APPLICANT:  McNabb, Andria
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.478C17
;  CURRENT APPLICATION NUMBER: US/09/902,941
;  CURRENT FILING DATE:  2001-07-10
;  NUMBER OF SEQ ID NOS: 2002
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 327
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-902-941-327

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RESULT 5
US-09-978-192A-322
; Sequence 322, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
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;  APPLICANT:  Kljavin, Ivar J.
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;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C9
;  CURRENT APPLICATION NUMBER: US/09/978,192A
;  CURRENT FILING DATE:  2001-10-15
;  PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 10; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
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RESULT 6
US-09-999-832A-322
; Sequence 322, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR APPLICATION NUMBER: 60/080327
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; PRIOR APPLICATION NUMBER: 60/080328
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; PRIOR APPLICATION NUMBER: 60/084414
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; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 10; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
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Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
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Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 7
US-09-849-626-327
; Sequence 327, Application US/09849626
; Publication No. US20020197669A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya
; APPLICANT: Fanger, Gary
; APPLICANT: Wang, Aijun
; APPLICANT: Wang, Tongtong
; APPLICANT: Switzer, Anne
; APPLICANT: McNeill, Patricia
; APPLICANT: Clapper, Jonathan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C16
; CURRENT APPLICATION NUMBER: US/09/849,626
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 1926
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-849-626-327

Query Match 100.0%; Score 784; DB 10; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
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Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 8
US-09-978-189-322
; Sequence 322, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15

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;  PRIOR APPLICATION NUMBER: 60/085579
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;  PRIOR APPLICATION NUMBER: 60/085580
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;  PRIOR APPLICATION NUMBER: 60/085573
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085704
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/085697

  Query Match             100.0%;  Score 784;  DB 11;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-78;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
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Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
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Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 9
US-09-978-608A-322
; Sequence 322, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C22
;  CURRENT APPLICATION NUMBER: US/09/978,608A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 322
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-608A-322

  Query Match             100.0%;  Score 784;  DB 11;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-78;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 10
US-09-978-585A-322
; Sequence 322, Application US/09978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C15
;  CURRENT APPLICATION NUMBER: US/09/978,585A
;  CURRENT FILING DATE:  2001-10-16
;  NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 322
;   LENGTH: 144
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-978-585A-322

  Query Match             100.0%;  Score 784;  DB 11;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-78;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
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Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144

RESULT 11
US-09-978-191A-322
; Sequence 322, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
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;  APPLICANT:  Napier, Mary A.
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;  APPLICANT:  Paoni, Nicholas F.
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;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C4
;  CURRENT APPLICATION NUMBER: US/09/978,191A
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Query Match 100.0%; Score 784; DB 11; Length 144;
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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
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;  TITLE OF INVENTION:  Acids Encoding the Same
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;  PRIOR FILING DATE: 1998-04-27
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; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 11; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
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Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
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Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 14
US-09-999-833A-322
; Sequence 322, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 11; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
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Qy          61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
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Db          61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy         121 CKLAFYLLAFFYYLYGMIYVLVSS 144
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RESULT 15
US-09-981-915A-322
; Sequence 322, Application US/09981915A
; Publication No. US20030054986A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi
;  APPLICANT:  Baker Kevin P.
;  APPLICANT:  Botstein, David
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Eaton, Dan
;  APPLICANT:  Ferrara, Napoleon
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Fong, Sherman
;  APPLICANT:  Gao, Wei-Qiang
;  APPLICANT:  Gerber, Hanspeter
;  APPLICANT:  Gerritsen, Mary E.
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Hillan, Kenneth J
;  APPLICANT:  Kljavin, Ivar J.
;  APPLICANT:  Kuo, Sophia S.
;  APPLICANT:  Napier, Mary A.
;  APPLICANT:  Pan, James;
;  APPLICANT:  Paoni, Nicholas F.
;  APPLICANT:  Roy, Margaret Ann
;  APPLICANT:  Shelton, David L.
;  APPLICANT:  Stewart, Timothy A.
;  APPLICANT:  Tumas, Daniel
;  APPLICANT:  Williams, P. Mickey
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;  TITLE OF INVENTION:  Acids Encoding the Same
;  FILE REFERENCE: P2630P1C12
;  CURRENT APPLICATION NUMBER: US/09/981,915A
;  CURRENT FILING DATE:  2001-10-16
;  PRIOR APPLICATION NUMBER: 09/918585
;  PRIOR FILING DATE: 2001-07-30
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; PRIOR APPLICATION NUMBER: 60/083336
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 784; DB 11; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.9e-78;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
```

Search completed: September 11, 2003, 14:51:37
Job time : 68 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 11, 2003, 14:26:30 ; Search time 86 Seconds
(without alignments)
265.775 Million cell updates/sec

Title: US-09-918-585A-322
Perfect score: 784
Sequence: 1 MAFTFAAFCYMLALLLTAAL.....FYLLAFFYYLYGMIYVLVSS 144

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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18: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA1997.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	784	100.0	144	20	AAY28813	pk65_4 secreted pr
2	784	100.0	144	20	AAY41306	Human cornichon pr
3	784	100.0	144	20	AAY41732	Human PRO181 prote
4	784	100.0	144	20	AAY32925	Transmembrane doma
5	784	100.0	144	21	AAB44288	Human PRO181 (UNQ1
6	784	100.0	144	21	AAB19524	Antitumour PRO181
7	784	100.0	144	22	AAM93330	Human polypeptide,
8	784	100.0	144	22	AAB76851	Human lung tumour
9	784	100.0	144	23	ABG31481	Human cornichon pr
10	784	100.0	144	23	ABB95423	Human angiogenesis
11	784	100.0	144	23	AAE20143	Human cornichon pr
12	784	100.0	144	23	AAU85506	Clone #19110 of lu
13	784	100.0	144	23	ABB84817	Human PRO181 prote
14	784	100.0	144	23	AAU83651	Human PRO protein,
15	784	100.0	144	24	ABU69478	Human lung cancer
16	784	100.0	144	24	ABU66380	Lung cancer therap
17	784	100.0	144	24	ABU61118	Human PRO181 polyp
18	784	100.0	144	24	ABU07410	Protein differenti
19	784	100.0	145	20	AAY04316	Human secreted pro
20	775	98.9	142	21	AAY53622	A bone marrow secr
21	586	74.7	160	22	AAB60464	Human cell cycle a
22	581	74.1	160	22	AAG89196	Human secreted pro
23	575	73.3	160	23	ABB97539	Novel human protei
24	573	73.1	161	21	AAY76218	Human secreted pro
25	548	69.9	144	22	ABB61865	Drosophila melanog
26	548	69.9	144	22	ABB61866	Drosophila melanog
27	381	48.6	104	22	AAM41565	Human polypeptide
28	321	40.9	80	22	AAM39779	Human polypeptide
29	244.5	31.2	139	21	AAY91543	Human secreted pro
30	244.5	31.2	139	21	AAY78803	Hydrophobic domain
31	244.5	31.2	139	22	AAM79013	Human protein SEQ
32	244.5	31.2	139	22	AAG89173	Human secreted pro
33	244.5	31.2	139	23	ABB89737	Human polypeptide
34	244.5	31.2	139	24	ABR47720	Human secreted pro
35	244.5	31.2	149	22	ABB12002	Human secreted pro
36	244.5	31.2	149	22	AAM79997	Human protein SEQ
37	244.5	31.2	155	21	AAY91689	Human secreted pro
38	244.5	31.2	160	22	AAM25811	Human protein sequ
39	230	29.3	45	20	AAY11505	Human 5' EST secre
40	196	25.0	35	20	AAY04330	Fragment of human
41	186.5	23.8	157	22	ABB70572	Drosophila melanog
42	175.5	22.4	137	21	AAG16801	Arabidopsis thalia
43	173	22.1	30	20	AAY04329	Fragment of human
44	167	21.3	30	20	AAY04328	Fragment of human
45	164.5	21.0	146	21	AAG15261	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAY28813
ID AAY28813 standard; Protein; 144 AA.
XX
AC AAY28813;
XX
DT 17-JAN-2000 (first entry)
XX
DE pk65_4 secreted protein.
XX
KW clone pk65_4; pk65_4 protein; human foetal kidney cDNA library;
KW secreted protein; transmembrane domain; cytokine; tissue growth;
KW TopPred II computer program; COS cell expression system;
KW membrane fraction; SDS polyacrylamide gel electrophoresis;
KW nutritional activity; cell proliferation; immune stimulation;
KW immune suppression; hematopoiesis regulation; tumour inhibition.
XX
OS Homo sapiens.
XX
PN WO9950405-A1.
XX
PD 07-OCT-1999.
XX
PF 30-MAR-1999; 99WO-US06946.
XX
PR 31-MAR-1998; 98US-0080110.
PR 29-MAR-1999; 99US-0280591.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, Mccoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Steininger RJ;

XX
DR WPI; 1999-610849/52.
DR N-PSDB; AAX90853.
XX
PT Polynucleotides encoding secreted human proteins, derived from human
PT adult brain, human fetal brain, human fetal kidney, and human adult
PT blood cDNA libraries -
XX
PS Claim 20; Page 105; 122pp; English.
XX
CC The present sequence is the pk65_4 secreted protein encoded by the cDNA
CC clone pk65_4. pk65_4 was isolated from a human foetal kidney cDNA
CC library using methods specific for secreted protein cDNAs. The TopPred II
CC computer program predicts three potential transmembrane domains within
CC the protein sequence, centered around amino acids 16, 67, and 133.
CC pk65_4 protein was expressed in a COS cell expression system, and an
CC expressed band of approximately 15kDa was detected in membrane fractions
CC using SDS polyacrylamide gel electrophoresis. The polynucleotide and
CC protein may effect nutritional activity, cytokine and cell proliferation,
CC immune stimulation or suppression, hematopoiesis regulation, tissue
CC growth, tumour inhibition etc.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 20; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
Db 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
Db 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy 121 CKLAFYLLAFFYYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFFYYLYGMIYVLVSS 144

RESULT 2
AAY41306
ID AAY41306 standard; Protein; 144 AA.
XX
AC AAY41306;
XX
DT 18-JAN-2000 (first entry)
XX
DE Human cornichon protein.
XX
KW Human; cornichon; differentiation; body plan; metazoan; oogenesis;
KW embryogenesis; dorsalization; oocyte; dorsal-ventral axis; bicoid;
KW anterior-posterior axis; microtubule; cytoskeleton; oskar; diagnosis;
KW developmental disorder; hereditary neuropathy ; seizure disorder;
KW reproductive disorder; immunological disorder; neoplastic disorder;
KW cancer; infection; spina biffida; cataract.
XX
OS Homo sapiens.
XX
PN US5968744-A.
XX
PD 19-OCT-1999.
XX
PF 14-OCT-1997; 97US-0950168.
XX
PR 14-OCT-1997; 97US-0950168.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Shah P, Corley NC;
XX
DR WPI; 1999-590398/50.
DR N-PSDB; AAZ30544.
XX
PT Isolated nucleic acids encoding human cornichon molecules, useful in
PT the recombinant production of cornichon proteins and in the prevention,
PT diagnosis and treatment of developmental, reproductive, immunological
PT and neoplastic disorders -
XX
PS Claim 1; Fig 1; 28pp; English.
XX
CC This sequence represents the human cornichon (CORN) protein (I). CORN
CC is involved in the differentiation and determination of body plan in
CC metazoans during oogenesis and embryogenesis. It is involved in
CC controlling the correct dorsalization of the oocyte (i.e. determining
CC the dorsal-ventral axis) and is essential in the correct induction of
CC the anterior-posterior axis. In this case, CORN is implicated in the
CC formation of correctly polarized microtubule cytoskeletons, which are
CC required for proper localization of the anterior and posterior
CC determinant genes (bicoid and oskar) and for the asymmetric positioning
CC of the oocyte nucleus (see Roth et al., Cell (1995)).
CC (I) may be used for the diagnosis, prevention and treatment of
CC disorders associated with inappropriate expression and/or activity of
CC CORN proteins. These disorders include developmental disorders (e.g.
CC anemia, Cushing's syndrome, epilepsy and achondroplastic dwarfism),
CC hereditary neuropathies (e.g. Charcot-Marie-Tooth disease), seizure
CC disorders (e.g. Syndenham's chorea and cerebral palsy), reproductive
CC disorders (e.g. infertility, disorders of prolactin production, tumors
CC and disruptions of the menstrual cycle), immunological disorders (e.g.
CC acquired immune deficiency syndrome (AIDS), Addison's disease and
CC asthma), neoplastic disorders (e.g. adenocarcinoma, leukemia, cancers
CC of the breast, lung, testis, ovaries and prostate and melanomas),
CC complications of cancers, bacterial, viral, parasitic, protozoal,
CC helminthic and fungal infections and other disorders such as spina
CC biffida and cataracts.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 20; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
Db 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
Db 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy 121 CKLAFYLLAFFYYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFFYYLYGMIYVLVSS 144

RESULT 3
AAY41732
ID AAY41732 standard; Protein; 144 AA.
XX
AC AAY41732;
XX
DT 07-DEC-1999 (first entry)
XX
DE Human PRO181 protein sequence.
XX
KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
KW secreted protein; transmembrane protein.
XX
OS Homo sapiens.
XX
PN WO9946281-A2.
XX
PD 16-SEP-1999.
XX

PF 08-MAR-1999; 99WO-US05028.
XX
PR 10-MAR-1998; 98US-0077450.
PR 11-MAR-1998; 98US-0077632.
PR 11-MAR-1998; 98US-0077641.
PR 11-MAR-1998; 98US-0077649.
PR 12-MAR-1998; 98US-0077791.
PR 13-MAR-1998; 98US-0078004.
PR 17-MAR-1998; 98US-0040220.
PR 20-MAR-1998; 98US-0078886.
PR 20-MAR-1998; 98US-0078910.
PR 20-MAR-1998; 98US-0078936.
PR 20-MAR-1998; 98US-0078939.
PR 25-MAR-1998; 98US-0079294.
PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079689.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 23-APR-1998; 98US-0082796.
PR 27-APR-1998; 98US-0083336.
PR 28-APR-1998; 98US-0083322.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.
PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH) GENENTECH INC.
XX
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AAZ34164.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
PS Claim 12; Fig 129; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AAZ33891 to
CC AAZ34338, and AAY41685 to AAY41774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 20; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
```

RESULT 4
AAY32925
ID AAY32925 standard; Protein; 144 AA.
XX
AC AAY32925;
XX
DT 04-NOV-1999 (first entry)
XX
DE Transmembrane domain containing protein clone HP02239.
XX
KW Transmembrane domain containing protein; human; antibody production;

KW interaction assay; diagnosis; nutritional activity; cytokine;
KW cell proliferation; cell differentiation activity; immune stimulant;
KW immune suppressant; haematopoiesis regulator; tissue growth activity;
KW activin; inhibin activity; chemotaxis; chemokinesis; haemostasis;
KW thrombolysis; anti-inflammatory; cadherin; tumour invasion suppressor;
KW tumour inhibitor.
XX
OS Homo sapiens.
XX
PN WO9943802-A2.
XX
PD 02-SEP-1999.
XX
PF 25-FEB-1999; 99WO-JP00875.
XX
PR 27-FEB-1998; 98JP-0046607.
XX
PA (PROT-) PROTEGENE INC.
PA (SAGA) SAGAMI CHEM RES CENT.
XX
PI Kato S, Kimura T, Nakamura N, Sekine S;
XX
DR WPI; 1999-527617/44.
DR N-PSDB; AAZ11179, AAZ11186.
XX
PT New proteins and DNA useful for preventing tumours
XX
PS Claim 1; Page 72-73; 96pp; English.
XX
CC This sequence is a human transmembrane protein of the invention. The
CC DNAs are useful for expressing recombinant protein for analysis,
CC characterisation or therapeutic use, and are useful as markers for
CC tissues in which the corresponding protein is preferentially expressed.
CC They are also useful as molecular weight markers on Southern gels, as
CC chromosome markers or tags (when labelled) to identify potential genetic
CC disorders, as probes to hybridise and thus discover novel, related DNA
CC sequences, as a source of PCR primers for genetic fingerprinting, as
CC probes to subtract-out known sequences in the process of discovering
CC other novel DNAs, for selecting and making oligomers for attachment to a
CC gene chip or other support, including for examination of expression
CC patterns, to raise anti-protein antibodies using DNA immunisation
CC techniques, and as an antigen to raise anti-DNA antibodies or elicit
CC another immune response. Where the DNA encodes a protein which binds to
CC another protein (e.g. in a receptor-ligand interaction), the DNA can also
CC be used in interaction trap assays to identify DNAs encoding the other
CC protein with which binding occurs or to identify inhibitors of the
CC binding interaction. The DNAs and proteins can have e.g. nutritional
CC activity, cytokine and cell proliferation/differentiation activity,
CC immune stimulating (e.g. as vaccines) or suppressing activity,
CC haematopoiesis regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC inhibition activity.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 20; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
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Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
```

RESULT 5
AAB44288
ID AAB44288 standard; Protein; 144 AA.
XX
AC AAB44288;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO181 (UNQ155) protein sequence SEQ ID NO:322.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
KW expressed sequence tag; detection; cancer.
XX
OS Homo sapiens.
XX
PN WO200053756-A2.
XX
PD 14-SEP-2000.
XX
PF 18-FEB-2000; 2000WO-US04341.
XX
PR 08-MAR-1999; 99WO-US05028.
PR 12-MAR-1999; 99US-0123957.
PR 29-MAR-1999; 99US-0126773.
PR 21-APR-1999; 99US-0130232.
PR 28-APR-1999; 99US-0131445.
PR 14-MAY-1999; 99US-0134287.
PR 23-JUN-1999; 99US-0141037.
PR 26-JUL-1999; 99US-0145698.
PR 29-OCT-1999; 99US-0162506.
PR 30-NOV-1999; 99WO-US28313.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28565.
PR 16-DEC-1999; 99WO-US30095.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31274.
PR 05-JAN-2000; 2000WO-US00219.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME;
PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
PI Kljavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA;
PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
XX
DR WPI; 2000-611443/58.
DR N-PSDB; AAC78538.
XX
PT Novel PRO polypeptides and polynucleotides used in detection methods,
PT to target bioactive molecules to specific cells, and to modulate
PT cellular activities -
XX
PS Claim 12; Fig 129; 636pp; English.
XX
CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
CC sequence tag) sequences which encode secreted or transmembrane PRO
CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
CC activity. The polynucleotides and polypeptides can be used for detecting
CC the presence of PRO polypeptides in samples, for linking bioactive
CC molecules to cells and for modulating biological activities of cells,
CC using the polypeptides for specific targeting. The polypeptide targeting
CC can be used to kill the target cells, e.g. for the treatment of cancers.
CC The polypeptide pairs provide specific targeting of bioactive molecules
CC to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
CC the isolation of the PRO polynucleotide sequences.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 21; Length 144;

```
  Best Local Similarity   100.0%;  Pred. No. 1.8e-85;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 6
AAB19524
ID   AAB19524 standard; Protein; 144 AA.
XX
AC   AAB19524;
XX
DT   09-JAN-2001  (first entry)
XX
DE   Antitumour PRO181 protein.
XX
KW   PRO181; antitumour; antiproliferative; human; cancer; therapy;
KW   drug screening.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..20
FT                   /label= Signal_peptide
FT   Domain          11..31
FT                   /label= Type-II_transmembrane_domain
FT   Domain          57..77
FT                   /label= Transmembrane_domain
FT   Domain          123..143
FT                   /label= Transmembrane_domain
FT   Modified-site   96..100
FT                   /note= "Glycosaminoglycan attachment site"
XX
PN   WO200053751-A1.
XX
PD   14-SEP-2000.
XX
PF   30-DEC-1999;   99WO-US31243.
XX
PR   08-MAR-1999;   99WO-US05028.
PR   29-MAR-1999;   99US-0126773.
PR   20-JUL-1999;   99US-0144758.
PR   08-SEP-1999;   99WO-US20594.
PR   20-DEC-1999;   99WO-US30999.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Ashkenazi AJ,  Baker KP,  Goddard A,  Gurney AL,  Napier MA,  Wood WI;
XX
DR   WPI; 2000-594321/56.
DR   N-PSDB; AAA88439.
XX
PT   Novel PRO181 and PRO237 polypeptides useful for treating tumors
PT   including cancers of breast, prostate, lung, leukemia in humans and for
PT   identifying compounds capable of inhibiting growth of neoplastic cells
PT   -
XX
PS   Claim 19; Fig 2; 107pp; English.
XX
CC   The present sequence is that of human PRO181 a novel inhibitor of
CC   neoplastic cell growth.  The sequence was deduced from a cDNA clone
CC   (see AAA88439) isolated from a placental cDNA library.  It shows
CC   significant sequence similarity to cornichon protein.  The
CC   invention provides PRO181 and PRO237 (see AAB19525) polypeptides and
CC   polynucleotides, vectors, host cells, methods for their production,
CC   chimeric molecules and antibodies.  Also claimed is a composition
CC   comprising PRO181 or PRO237, or their agonists, useful for the
CC   treatment of a tumour, especially breast cancer, ovarian cancer,
CC   renal cancer, colorectal cancer, uterine cancer, prostate cancer,
CC   lung cancer, bladder cancer, central nervous system cancer,
CC   melanoma and leukaemia.  PRO181 and PRO237 are also useful for
CC   treating neuronal, glial, astrocytal, hypothalamic and other
CC   glandular, macrophagal, epithelial, stromal, and blastocoelic
CC   disorders and inflammatory, angiogenic and immunologic disorders.
CC   They are useful for identifying agonists to PRO181 or PRO237 in
CC   drug screening and rational drug design.
XX
SQ   Sequence   144 AA;

  Query Match             100.0%;  Score 784;  DB 21;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-85;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 7
AAM93330
ID   AAM93330 standard; Protein; 144 AA.
XX
AC   AAM93330;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polypeptide, SEQ ID NO: 2859.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   N-PSDB; AAK94250.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Claim 8; SEQ ID NO 2859; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
```

CC molecules have been determined. Primers for synthesising the full length
CC cDNA are useful for clarifying the function of the protein encoded by
CC the cDNA. The full length clones were obtained by construction of full
CC length enriched cDNA libraries that were synthesised by the oligo-capping
CC method. The primers enable the production of the full length cDNA easily
CC without any special methods. The present sequence is a polypeptide
CC encoded by a full length human cDNA of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 22; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
Db 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
Db 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy 121 CKLAFYLLAFFYYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFFYYLYGMIYVLVSS 144

RESULT 8
AAB76851
ID AAB76851 standard; Protein; 144 AA.
XX
AC AAB76851;
XX
DT 12-APR-2001 (first entry)
XX
DE Human lung tumour protein related protein sequence SEQ ID NO:327.
XX
KW Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KW lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KW cytostatic; antisense inhibition.
XX
OS Homo sapiens.
XX
PN WO200100828-A2.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18061.
XX
PR 30-JUN-1999; 99US-0346492.
PR 15-OCT-1999; 99US-0419356.
PR 17-DEC-1999; 99US-0466867.
PR 30-DEC-1999; 99US-0476300.
PR 06-MAR-2000; 2000US-0519642.
PR 22-MAR-2000; 2000US-0533077.
PR 10-APR-2000; 2000US-0546259.
PR 27-APR-2000; 2000US-0560406.
PR 05-JUN-2000; 2000US-0589184.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;
XX
DR WPI; 2001-071488/08.
XX
PT Lung tumor-associated proteins and the nucleic acids that encode them,
PT useful for preventing, diagnosing and treating lung cancer -
XX
PS Example 1; Page 254; 436pp; English.
XX

CC The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them.
CC (I) have cytostatic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the protein by expressing inactive proteins
CC or to supplement the patients own production of (I). Additionally, the
CC NAs may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC samples, and hence which patients may be in need of treatment for lung
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF68878 and
CC AAB76848 to AAB76878 represent human lung tumour protein related
CC nucleotide and protein sequences which are used in the exemplification
CC of the present invention.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 22; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
Db 1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
Db 61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy 121 CKLAFYLLAFFYYLYGMIYVLVSS 144
Db 121 CKLAFYLLAFFYYLYGMIYVLVSS 144

RESULT 9
ABG31481
ID ABG31481 standard; Protein; 144 AA.
XX
AC ABG31481;
XX
DT 20-NOV-2002 (first entry)
XX
DE Human cornichon protein (CORN).
XX
KW Human; cornichon protein; CORN; bladder cDNA library; BLADNOT04;
KW Incyte clone 1318847; developmental disorder; reproductive disorder;
KW immunological disorder; autoimmune disorder; neoplastic disorder;
KW microarray; cytostatic; antiinflammatory; gynaecological;
KW immunosuppressive.
XX
OS Homo sapiens.
XX
PN US2002103342-A1.
XX
PD 01-AUG-2002.
XX
PF 10-JAN-2002; 2002US-0044477.
XX
PR 14-OCT-1997; 97US-0950168.
PR 02-AUG-1999; 99US-0365705.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Hillman JL, Corley NC, Shah P;

XX
DR WPI; 2002-690628/74.
DR N-PSDB; ABK91098.
XX
PT New human cornichon protein and polynucleotide for diagnosing,
PT preventing or treating developmental, reproductive, immunological, and
PT neoplastic disorders -
XX
PS Claim 1; Fig 1; 32pp; English.
XX
CC The present invention relates to the isolation of human cornichon
CC protein (CORN), and the polynucleotide sequence encoding it. The
CC sequences are isolated from bladder cDNA library (BLADNOT04) Incyte
CC clone 1318847. The polynucleotide and polypeptide sequences for
CC CORN are useful in the diagnosis, prevention, and treatment of
CC developmental disorders (e.g. anaemia, renal tubular acidosis,
CC Cushing's syndrome, dwarfism, epilepsy, hypothyroidism, glaucoma,
CC sensorineural hearing loss and cataract), reproductive disorders
CC (e.g. disorders of prolactin production, infertility, endometriosis,
CC polycystic ovary syndrome, endometrial and ovarian tumours, ectopic
CC pregnancy, prostate cancer, prostatitis, and carcinoma of the male
CC breast and gynaecomastia), immunological disorders (e.g. autoimmune
CC disorders, acquired immunodeficiency syndrome (AIDS), adult
CC respiratory distress syndrome, Addison's disease, allergies, anaemia,
CC asthma, atherosclerosis, gout, myocardial or pericardial inflammation,
CC osteoporosis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, ulcerative colitis, haemodialysis, Crohn's disease,
CC atopic dermatitis, autoimmune thyroiditis, diabetes mellitus, Graves'
CC disease, glomerulonephritis, viral, bacterial, fungal, parasitic,
CC protozoal, helminthic infections and trauma), and neoplastic disorders
CC (e.g. adenocarcinoma, leukaemia, lymphoma, melanoma, and various
CC cancers). CORN, fragments of CORN, and antibodies specific for CORN
CC are useful as elements on a microarray which is useful to monitor or
CC measure protein-protein interactions, drug-target interactions and
CC gene expression profiles. The present sequence represents human CORN.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 23; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
```

RESULT 10
ABB95423
ID ABB95423 standard; Protein; 144 AA.
XX
AC ABB95423;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO181 SEQ ID NO: 2.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US21735.
XX
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 15-SEP-2000; 2000US-000000P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 28-JUN-2001; 2001WO-US00000.
XX
PA (GETH) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERR/) FERRARA N.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J F.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-171999/22.
DR N-PSDB; ABL95561.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 2; 567pp; English.
XX

```
CC   The present invention provides the protein and coding sequences of human
CC   PRO proteins. These are useful for treating or diagnosing a
CC   cardiovascular, endothelial or angiogenic disorder, including cardiac
CC   hypertrophy, trauma, cancer, age-related macular degeneration,
CC   atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
CC   angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
CC   angiogenesis (such as breast carcinoma and liver carcinoma) and wound
CC   healing. The present sequence is a PRO protein of the invention.
XX
SQ   Sequence   144 AA;

  Query Match             100.0%;  Score 784;  DB 23;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-85;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 11
AAE20143
ID   AAE20143 standard; Protein; 144 AA.
XX
AC   AAE20143;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human cornichon protein (CORN).
XX
KW   Human; cornichon protein; CORN; Cushing's syndrome; muscular dystrophy;
KW   developmental disorder; neoplastic; seizure; reproductive; immunological;
KW   tubular acidosis; anaemia; polycystic ovary; autoimmune disorder; tumour;
KW   breast cancer; prostate; testis; epilepsy; neuropathy; Addison's disease;
KW   ulcerative colitis; spermatogenesis; hypothyroidism; cataract; arthritis;
KW   infertility; galactorrhea; gynaecomastia; diabetes mellitus; fungicide;
KW   dermatitis; acquired immunodeficiency syndrome; AIDS; glomerulonephritis;
KW   atherosclerosis; allergy; asthma; bronchitis; Crohn's disease; auditory;
KW   gout; Graves' disease; multiple sclerosis; haemodialysis; anticonvulsant;
KW   trauma; drug screening; ophthalmological; cytostatic; immunosuppressive;
KW   gynaecological; antiulcer; nephrotropic; neuroprotective; antihelmintic;
KW   antibacterial; tranquillizer; osteoporosis; antiparasitic; protozoacide;
KW   vulnerary; virucide; gene therapy.
XX
OS   Homo sapiens.
XX
PN   US6348576-B1.
XX
PD   19-FEB-2002.
XX
PF   02-AUG-1999;   99US-0365705.
XX
PR   14-OCT-1997;   97US-0950168.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Hillman JL,  Corley NC,  Shah P;
XX
DR   WPI; 2002-266544/31.
DR   N-PSDB; AAD31079.
XX
PT   New human cornichon protein, useful for diagnosis, prevention and
PT   treatment of developmental, reproductive, immunological and neoplastic
PT   disorders and to screen for molecules that bind the protein  -
XX
PS   Claim 1; Fig 2; 29pp; English.
XX
CC   The invention relates to a purified human cornichon protein (CORN). CORN
CC   is useful for diagnosis, prevention and treatment of developmental,
CC   reproductive, immunological and neoplastic disorders. Developmental
CC   disorders include renal tubular acidosis, anaemia, Cushing's syndrome,
CC   achondroplastic dwarfism, Duchenne and Becker muscular dystrophy,
CC   epilepsy, hereditary neuropathies such as Charcot-Marie-Tooth disease,
CC   neurofibromatosis, hypothyroidism, seizure disorders such as cerebral
CC   palsy, cataract and sensorineural hearing loss and reproductive disorders
CC   include disorders of prolactin production, infertility, ovulatory
CC   defects, endometriosis, disruptions of the oestrous cycle, disruptions of
CC   the menstrual cycle, polycystic ovary syndrome, endometrial and ovarian
CC   tumours, autoimmune disorders, ectopic pregnancy, cancer of the breast,
CC   galactorrhea, disruptions of spermatogenesis, cancer of the testis,
CC   cancer of the prostate, prostatitis and carcinoma of the male breast and
CC   gynaecomastia. Immunological disorders include acquired immunodeficiency
CC   syndrome (AIDS), diabetes mellitus, arthritis, including rheumatoid
CC   arthritis, osteoarthritis, Addison's disease, allergies, asthma,
CC   atherosclerosis, bronchitis, Crohn's disease, ulcerative colitis, atopic
CC   dermatitis, glomerulonephritis, gout, Graves' disease, multiple
CC   sclerosis, osteoporosis, autoimmune thyroiditis, complications of cancer,
CC   haemodialysis and extracorporeal circulation, viral, bacterial, fungal,
CC   parasitic, protozoal and helminthic infections, and trauma. CORN, is
CC   catalytic or immunogenic fragments is useful for screening libraries of
CC   compounds in a variety of drug screening techniques. The present
CC   sequence is human CORN. CORN gene is useful in gene therapy.
XX
SQ   Sequence   144 AA;

  Query Match             100.0%;  Score 784;  DB 23;  Length 144;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-85;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 12
AAU85506
ID   AAU85506 standard; Protein; 144 AA.
XX
AC   AAU85506;
XX
DT   21-MAY-2002  (first entry)
XX
DE   Clone #19110 of lung tumour protein.
XX
KW   Lung tumour; cancer; T cell; immune response stimulator;
KW   cytostatic.
XX
OS   Homo sapiens.
XX
PN   WO200204514-A2.
XX
PD   17-JAN-2002.
XX
PF   10-JUL-2001; 2001WO-US22058.
XX
PR   11-JUL-2000; 2000US-0614124.
PR   29-AUG-2000; 2000US-0651563.
PR   08-SEP-2000; 2000US-0658824.
PR   26-SEP-2000; 2000US-0671325.
PR   06-OCT-2000; 2000US-0677419.
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PR 30-OCT-2000; 2000US-0702705.
PR 13-DEC-2000; 2000US-0736457.
PR 03-MAY-2001; 2001US-0849626.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Marnerakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS;
PI Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
XX
DR WPI; 2002-164634/21.
DR N-PSDB; ABK38061.
XX
PT Novel polynucleotide encoding a lung tumour polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumour protein -
XX
PS Example 1; SEQ ID No 327; 223pp; English.
XX
CC The invention describes an isolated polynucleotide and polypeptide
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein for determining the presence of a cancer in a patient. A
CC composition containing the polynucleotide and/or polypeptide is useful
CC for treating a lung cancer in a patient. The polypeptide is useful for
CC removing tumour cells from a biological sample. The polynucleotide is
CC also useful as probe or primer to detect the level of mRNA encoding a
CC tumour protein. This is the amino acid sequence of a lung tumour
CC associated protein, described in the method of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 23; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
```

RESULT 13
ABB84817
ID ABB84817 standard; Protein; 144 AA.
XX
AC ABB84817;
XX
DT 16-MAY-2002 (first entry)
XX
DE Human PRO181 protein sequence SEQ ID NO:2.
XX
KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
KW vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;
KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
KW age-related macular degeneration; arterial restenosis; angina;
KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
KW wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN WO200200690-A2.
XX
PD 03-JAN-2002.
XX
PF 20-JUN-2001; 2001WO-US19692.
XX
PR 23-JUN-2000; 2000US-213637P.
PR 20-JUL-2000; 2000US-219556P.
PR 25-JUL-2000; 2000US-220624P.
PR 25-JUL-2000; 2000US-220664P.
PR 28-JUL-2000; 2000WO-US20710.
PR 02-AUG-2000; 2000US-222695P.
PR 17-AUG-2000; 2000US-0643657.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 07-SEP-2000; 2000US-230978P.
PR 18-SEP-2000; 2000US-0664610.
PR 18-SEP-2000; 2000US-0665350.
PR 24-OCT-2000; 2000US-242922P.
PR 08-NOV-2000; 2000US-0709238.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000US-0747259.
PR 20-DEC-2000; 2000WO-US34956.
PR 22-JAN-2001; 2001US-0767609.
PR 28-FEB-2001; 2001US-0796498.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 09-MAR-2001; 2001US-0802706.
PR 14-MAR-2001; 2001US-0808689.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0828366.
PR 10-MAY-2001; 2001US-0854208.
PR 10-MAY-2001; 2001US-0854280.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 25-MAY-2001; 2001WO-US17092.
PR 30-MAY-2001; 2001US-0870574.
PR 30-MAY-2001; 2001WO-US17443.
PR 01-JUN-2001; 2001WO-US17800.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
XX
DR WPI; 2002-090516/12.
DR N-PSDB; ABL88072.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal -
XX
PS Claim 11; Fig 2; 565pp; English.
XX
CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
CC activities, and can be used in gene therapy. The PRO polynucleotides,
CC proteins, agonists and antagonists are useful for treating or diagnosing
CC a cardiovascular, endothelial or angiogenic disorder in a mammal,
CC e.g. cardiac hypertrophy, trauma, cancer, age-related macular
CC degeneration, atherosclerosis, hypertension, arterial restenosis,
CC rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
CC lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
CC carcinoma) and wound healing. The PRO polynucleotides have applications
CC in molecular biology, including use as hybridisation probes, and in
CC chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
CC probes used in the exemplification of the present invention.
XX
SQ Sequence 144 AA;

```
  Query Match           100.0%;  Score 784;  DB 23;  Length 144;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-85;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 14
AAU83651
ID   AAU83651 standard; Protein; 144 AA.
XX
AC   AAU83651;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human PRO protein, Seq ID No 120.
XX
KW   Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW   breast cancer; prostate tumour; rectal tumour; liver tumour;
KW   pericyte cell proliferation; chondrocyte cell proliferation;
KW   tumour necrosis factor-alpha.
XX
OS   Homo sapiens.
XX
PN   WO200208288-A2.
XX
PD   31-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US21066.
XX
PR   20-JUL-2000; 2000US-219556P.
PR   25-JUL-2000; 2000US-220585P.
PR   25-JUL-2000; 2000US-220605P.
PR   25-JUL-2000; 2000US-220607P.
PR   25-JUL-2000; 2000US-220624P.
PR   25-JUL-2000; 2000US-220638P.
PR   25-JUL-2000; 2000US-220664P.
PR   25-JUL-2000; 2000US-220666P.
PR   26-JUL-2000; 2000US-220893P.
PR   28-JUL-2000; 2000WO-US20710.
PR   23-AUG-2000; 2000WO-US23522.
PR   24-AUG-2000; 2000WO-US23328.
PR   15-SEP-2000; 2000US-000000P.
PR   10-NOV-2000; 2000WO-US30873.
PR   28-NOV-2000; 2000US-253646P.
PR   01-DEC-2000; 2000WO-US32678.
PR   20-DEC-2000; 2000US-0747259.
PR   20-DEC-2000; 2000WO-US34956.
PR   28-FEB-2001; 2001WO-US06520.
PR   10-MAY-2001; 2001US-0854280.
PR   25-MAY-2001; 2001WO-US17092.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Desnoyers L,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Smith V,  Stephan JF,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2002-172001/22.
DR   N-PSDB; ABK33595.
XX
PT   One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT   useful for treating a PRO related disorder and for diagnosing tumours
PT   such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
PT   tumour or liver tumour -
XX
PS   Claim 11; Figure 120; 359pp; English.
XX
CC   The invention relates to one hundred and twenty two nucleic acids
CC   encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC   encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC   agonists and antagonists are useful for treating a PRO related disorder.
CC   The PRO polypeptides are useful for diagnosing tumours, especially lung
CC   cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC   liver tumour. The PRO polypeptides are useful for stimulating the
CC   proliferation of, or gene expression, in pericyte cells, for stimulating
CC   the proliferation or differentiation of chondrocyte cells, for
CC   stimulating the release of tumour necrosis factor-alpha from human blood,
CC   for stimulating or inhibiting the proliferation of normal human dermal
CC   fibroblast cells. The PRO polypeptide may also be used as molecular
CC   weight markers and for tissue typing. The PRO nucleic acids have
CC   applications in molecular biology, including use as hybridisation probes,
CC   and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC   protein sequences of the invention.
XX
SQ   Sequence   144 AA;

  Query Match           100.0%;  Score 784;  DB 23;  Length 144;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-85;
  Matches  144;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144


RESULT 15
ABU69478
ID   ABU69478 standard; Protein; 144 AA.
XX
AC   ABU69478;
XX
DT   05-JUN-2003  (first entry)
XX
DE   Human lung cancer associated cDNA #19110 protein.
XX
KW   Human; lung cancer; lung tumour; cytostatic; vaccine;
KW   T cell expansion; CD4; CD8.
XX
OS   Homo sapiens.
XX
PN   US2002197669-A1.
XX
PD   26-DEC-2002.
XX
PF   03-MAY-2001; 2001US-0849626.
XX
PR   13-DEC-2000; 2000US-0736457.
XX
PA   (BANG/) BANGUR C S.
PA   (FANG/) FANGER G R.
PA   (WANG/) WANG A.
PA   (WANG/) WANG T.
PA   (SWIT/) SWITZER A P.
PA   (MCNE/) MCNEILL P D.
PA   (CLAP/) CLAPPER J D.
XX
PI   Bangur CS,  Fanger GR,  Wang A,  Wang T,  Switzer AP,  McNeill PD;
PI   Clapper JD;
```

XX
DR WPI; 2003-352750/33.
DR N-PSDB; ACA10390.
XX
PT Novel lung cancer polynucleotide encoding lung cancer protein, useful
PT for detecting the presence of lung cancer in a patient, and in
PT pharmaceutical compositions, e.g. vaccines, for treating lung cancer -
XX
PS Example 1; Page -; 72pp; English.
XX
CC The invention relates to a polynucleotide encoding a lung tumour protein,
CC comprising a sequence selected from any of the 14 sequences
CC mentioned in the specification, or a sequence (S2) mentioned in
CC specification, complement of S1, sequences consisting of at least 20
CC contiguous residues of S1, sequences that hybridise to S1, sequences
CC having 75%, preferably 90%, identity to S1, or degenerate variants of
CC S1. Also included are an isolated polypeptide (comprising a sequence (S3)
CC selected from any one of the 4 amino acid sequences mentioned in the
CC specification, a sequence encoded by the polynucleotide, or sequences
CC having at least 70%, preferably 90%, identity to a sequence encoded by
CC the polynucleotide), an expression vector comprising the polynucleotide
CC operably linked to an expression control sequence, a host cell
CC transformed or transfected with the vector, an isolated antibody (or its
CC antigen-binding fragment) that specifically binds to the polypeptide,
CC detecting the presence of a cancer in a patient, a fusion protein
CC comprising the polypeptide, an oligonucleotide that hybridises to
CC S1 under moderately stringent conditions, stimulating and/or expanding T
CC cells specific for a tumour protein (comprising contacting T cells with
CC the polynucleotide, protein or antigen-presenting cells, under conditions
CC and for a time sufficient to permit the stimulation and/or expansion of T
CC cells) and inhibiting the development of a cancer in a patient (by
CC incubating CD4^+ and/or CD8^+ T cells isolated from a patient with the
CC polynucleotide, protein or antigen presenting cells that express the
CC polynucleotide, such that T cells proliferate, administering to the
CC patient an effective amount of the proliferated T cells, and thus
CC inhibiting the development of a cancer in the patient. The
CC polynucleotide, protein ands cells are useful in a composition for
CC stimulating an immune response in a patient, and for treating a cancer in
CC a patient (particularly lung cancer). The oligonucleotide is useful for
CC determining the presence of a cancer in a patient. The protein and
CC oligonucleotides are useful in pharmaceutical compositions, e.g.
CC vaccines. The polynucleotide is also useful as a probe or primer for
CC nucleic acid hybridisation, and in the design and preparation of
CC ribozyme molecules for inhibiting expression of tumour polypeptides and
CC proteins in tumour cells. An amplified portion of the polynucleotide is
CC useful for isolating a full-length gene from a suitable library.
CC The present sequence is a protein encoded by a cDNA (full length,
CC extended or partial) isolated from a library derived from lung tumour/
CC cancer cells.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from the USPTO
CC at seqdata.uspto.gov/sequence.html?DocId=20020197669.
XX
SQ Sequence 144 AA;

Query Match 100.0%; Score 784; DB 24; Length 144;
Best Local Similarity 100.0%; Pred. No. 1.8e-85;
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAFTFAAFCYMLALLLTAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHA 60

Qy         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FFCVMFLCAAEWLTLGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGW 120

Qy        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
              ||||||||||||||||||||||||
Db        121 CKLAFYLLAFFYYLYGMIYVLVSS 144
```

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